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Holly Schnizer
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305-3722
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Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
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Full text: _____
Patent Family: _____
Other: _____

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WWW/Internet: _____
Other (specify): _____

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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 17 Seconds

(without alignments)
824.350 Million cell updates/sec

Title: US-09-185-904A-33

Perfect score: 1543
Sequence: 1 MTEQALISPAKFLAGIAAA.....LRMGAFVLVYDELKKVI 298

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	1 ADT3_HUMAN	P12236 homo sapien
2	1512	98.0	298	1 ADT3_BOVIN	P32007 bos taurus
3	1463	94.8	298	1 ADT2_HUMAN	P08141 homo sapien
4	1451	94.0	298	1 ADT2_RAT	P08073 rattus norv
5	1445	93.6	298	1 ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	1 ADT1_RAT	Q05962 rattus norv
7	1418	91.9	298	1 ADT1_MOUSE	P49962 bos taurus
8	1417	91.8	297	1 ADT1_BOVIN	P02722 bos taurus
9	1409	91.3	298	1 ADT1_HUMAN	P12235 homo sapien
10	1254.5	81.3	299	1 ADT1_MOUSE	Q26365 drosophila
11	1204	78.0	301	1 ADT1_MOUSE	Q27238 anopheles g
12	978	63.4	339	1 ADT1_MOUSE	P31692 chlorella x
13	778.5	50.5	307	1 ADT3_YEAST	P18238 saccharomyc
14	772	50.0	308	1 ADT1_CHICK	P27028 chlamydomon
15	769	49.8	322	1 ADT1_SCHPO	O09188 schizosacch
16	768	49.8	386	1 ADT1_GOSHI	O23342 gossypium h
17	766	49.6	313	1 ADT1_NEUCR	P03723 neurospora
18	762.5	49.4	305	1 ADT1_KUTLA	P49382 kluyveromyc
19	760.5	49.3	318	1 ADT2_YEAST	P18239 saccharomyc
20	750.5	48.6	385	1 ADT2_ARATH	P40941 arabidopsis
21	750	48.6	387	1 ADT1_MAIZE	P04709 zea mays (m
22	748	48.5	386	1 ADT1_SOLITU	P25083 solanum tub
23	747	48.4	382	1 ADT1_OBYSA	P13691 oryza sativ
24	744	48.2	387	1 ADT2_MAIZE	P18857 zea mays (m
25	742.5	48.1	381	1 ADT1_ARATH	P31667 arabidopsis
26	740	48.0	331	1 ADT1_ARATH	Q41629 triticum ae
27	739.5	47.9	386	1 ADT2_SOLITU	P27081 solanum tub
28	737.5	47.8	309	1 ADT1_YEAST	P04710 saccharomyc
29	727	47.1	331	1 ADT2_WHEAT	Q41630 triticum ae
30	305.5	19.8	565	1 CMG2_CAEEL	Q15529 caenorhabdi
31	302	19.6	588	1 CMG2_CAEEL	Q20799 caenorhabdi
32	300	19.4	330	1 GDC_BOVIN	Q01888 bos taurus
33	299	19.4	307	1 ODC2_YEAST	Q99297 saccharomyc

34	295	19.1	678	1 CMG1_HUMAN	O75746 homo sapien
35	289.5	18.8	322	1 GDC_RAT	P16261 rattus norv
36	289.5	18.6	702	1 CMG1_CAEEL	O21153 caenorhabdi
37	286	18.5	325	1 UCPS_HUMAN	O95258 homo sapien
38	285	18.5	332	1 GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1 UCPS_MOUSE	Q942b2 mus musculu
40	282.5	18.3	326	1 YE08_SCHPO	O13805 schizosacch
41	280	18.1	675	1 CMG2_HUMAN	O942b0 homo sapien
42	272	17.6	315	1 MFT_HUMAN	O942d1 homo sapien
43	270	17.5	315	1 SNA1_HUMAN	O941k4 homo sapien
44	265	17.2	312	1 UCPS_HUMAN	P55916 homo sapien
45	265	17.2	676	1 CMG2_MOUSE	Q94qxx4 mus musculu

ALIGNMENTS

RESULT 1
ADT3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; O96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
CN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
ADP/ATP translocase.";
RL 1 Mol Biol 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RN Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueding T.B., Toshitsuki S., Canninci P., Prange C.,
RA Bata S.S., Lequellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Roha S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Binkley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherter A., Schein J.B., Jones S.J.W., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

```

RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03592; AAA6750.1; -.
DR EMBL: AY007135; AAG01998.1; -.
DR EMBL: BC007285; AAH07285.1; -.
DR EMBL: BC007850; AAH07850.1; -.
DR EMBL: BC008737; AAH08737.1; -.
DR EMBL: BC008935; AAH08935.1; -.
DR EMBL: BC014775; AAH14775.1; -.
DR PIR: S03894; S03894.
DR Genew: HGNC:10992; SLC25A6.
DR MIM: 300151; -.
DR MIM: 403000; -.
DR GO: GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
DR GO: GO:0005471; F:ATP/ADP antiporter activity; NAS.
DR GO: GO:0006854; P:ATP/ADP exchange; TAS.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PRINTS: PRO0784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT REPEAT 105 108 3.
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3; De-128;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 OSGRKGADIMVTGTVDCWKRIFPDEGGKAFPKGAMSVNLKMGGAFLVLYDELKKVI 298
DB 241 OSGRKGADIMVTGTVDCWKRIFPDEGGKAFPKGAMSVNLKMGGAFLVLYDELKKVI 298

RESULT 2
ADT3 BOVIN STANDARD; PRT; 298 AA.
AC P32067;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; Pubmed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.B.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL: M24103; AAA30769.1; -.
DR PTR: B43646; B43646.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PRINTS: PRO0784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 98.0%; Score 1512; DB 1; Length 298;
Best Local Similarity 97.7%; Pred. No. 1; 9e-125;
Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY 61 IPKEGVLSFWKGNLAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKEGVLSFWKGNLAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFTRTLADVKGSGTEREFGDGLVTKTSQDGRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFTRTLADVKGSGTEREFGDGLVTKTSQDGRGLYOGFSVS 180
 QY 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAVAGVSYFPDTRRRMM 240
 DB 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAVAGVSYFPDTRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWRKIFDEGGAFFKGAWSNVLRGSGAFVLYVDELKVI 298
 DB 241 QSGRKGADIMYTGTVDCWRKIFDEGGAFFKGAWSNVLRGSGAFVLYVDELKVI 298

RESULT 3
 ADT2 HUMAN STANDARD; PRT; 298 AA.
 ID ADT2 HUMAN STANDARD; PRT; 298 AA.
 AC P05141; 043350;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 GN (Adenine nucleotide translocator 2) (ANT 2).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90375457; PubMed=2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Basesga R., Murrel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=87166056; PubMed=3031073;
 RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
 RA Basesga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 growth-regulated.";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Chen C.N., Su Y., Baybayan P., Siruno A., Nagataja R.,
 RA Mazarella R.A., Schlesinger D., Chen E.Y.;
 RT Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC Becker M., Graves T., Ozerky P.;
 RT Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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DR EMBL; M57424; AAA51737.1; -;
 DR EMBL; J02683; AAA35579.1; -;
 DR EMBL; L78810; AAB39266.1; -;
 DR EMBL; AC004000; AAB96347.1; -;
 DR EMBL; J03591; AAA6749.1; -;
 DR PIR; A29132; A29132.
 DR Gene; HGNC:10991; SLC25A5.
 DR MIM; 300150;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0015207; F:adenine transporter activity; TAS.
 DR GO; GO:0006832; P:small molecule transport; TAS.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR001993; Mit_uncoupling.
 DR InterPro; IPR001993; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MM; F973G3ARD92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;
 Best Local Similarity 92.9%; Pred. No. 3.8e-121;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTEQASIFADFLAGIAAIAISKTAVAPIERVKLLQVQASQKQIADKQYKGIYDCIVR 60
 DB 1 MTEQASIFADFLAGIAAIAISKTAVAPIERVKLLQVQASQKQIADKQYKGIYDCIVR 60
 QY 61 IPKEGVLSFWKGNLAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKEGVLSFWKGNLAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFTRTLADVKGSGTEREFGDGLVTKTSQDGRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFTRTLADVKGSGTEREFGDGLVTKTSQDGRGLYOGFSVS 180
 QY 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAVAGVSYFPDTRRRMM 240
 DB 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAVAGVSYFPDTRRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWRKIFDEGGAFFKGAWSNVLRGSGAFVLYVDELKVI 298
 DB 241 QSGRKGADIMYTGTVDCWRKIFDEGGAFFKGAWSNVLRGSGAFVLYVDELKVI 298

RESULT 4
 ADT2 RAT STANDARD; PRT; 298 AA.
 ID ADT2 RAT STANDARD; PRT; 298 AA.
 AC Q09073;
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLIC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN
 RP
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC -----
 DR EMBL; D12771; BAA02238.1; -;
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR InterPro; IPR001993; Mito_carrier.
 DR Pfam; PF00153; mltc_carri; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFB35 CRC64;
 Query March 94.0%; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.9%; Pred. No. 4.3e-120; Indels 0; Gaps 0;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAI SPADKFLAGIAIAAISKTA VAVPIERVKLLLOVHASKOIAADKOYGI VDCIVR 60
 DB 1 MTDAAVSPADKFLAGIAIAAISKTA VAVPIERVKLLLOVHASKOITD KOYKGI IDCVR 60
 QY 61 IPKQGVLSFWRGMLAVIRYFPFOALNFAFKDYKYOIFLGGVDKHTQFWRYFAGNLA SG 120
 DB 61 IPKQGVLSFWRGMLAVIRYFPFOALNFAFKDYKYOIFLGGVDKHTQFWRYFAGNLA SG 120
 QY 121 GAGGATSLCPYYPIDPAATRLAAVVGSGTEREFGAGDCLVKTSGDGRGLVQSGFVS 180
 DB 121 GAGGATSLCPYYPIDPAATRLAAVVGSGTEREFGAGDCLVKTSGDGRGLVQSGFVS 180
 QY 181 VGGIIIVRAAVFGVYDTAKGMLDPDKNTHIVSWMLAQTVAVAGVVSYPEDTVRRMM 240

DB 181 VGGIIIVRAAVFGVYDTAKGMLDPDKNTHIVSWMLAQSVTAVAGLTSYFPDTVRRMM 240
 QY 241 QSGRKADIVYTQVQWKRIFPRDEGKAFFKAMSVLVJGMDGAPFLVLYDEIAK 296
 DB 241 QSGRKADIVYTQVQWKRIFPRDEGKAFFKAMSVLVJGMDGAPFLVLYDEIAK 296
 RESULT 5
 ID ADT2_MOUSE STANDARD; PRT; 298 AA.
 AC P51881; Q61311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 26-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLIC25A5 OR ANT2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN
 RP
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RT homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995), University of Cambridge, U.K.
 RN
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Coster P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC -----
 DR EMBL; U27316; AAC52838.1; -;
 DR EMBL; U10404; AAA19009.1; -;
 DR EMBL; X70847; CAA50196.1; -;
 DR EMBL; AF240003; AAF64471.1; -;
 DR MGD; MGI:1353496; SLIC25a5.
 DR InterPro; IPR002067; Mlt_carrier.

DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUOCOUPLING.
 DR PROSITE; PS00215; MITOCH CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EE20 CRC64;

Query Match 93.6%; Score 1445; DB 1; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.4e-119;
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISKTAVPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60
 DB 1 MTDAAVFAKDFLAGGVAIAISKTAVPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
 QY 61 IPKEGQVSPFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVHGTQFMRFFAGNLSG 120
 DB 61 IPKEGQVSPFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVHGTQFMRFFAGNLSG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLVKITKSDIGRLYGQFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLVKITKSDIGRLYGQFSVS 180
 QY 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAQTVAAGVSYPPDYRRRRMM 240
 DB 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIFISWMIAGSVTAAGLTSYPPDYRRRRMM 240
 QY 241 QSGRGADIMTGTGVDCKRKIFRDEGKAFKFGKANSNVLKMGCAFVLVYDELKVI 298
 DB 241 QSGRGADIMTGTGVDCKRKIFRDEGKAFKFGKANSNVLKMGCAFVLVYDELKVI 298

RESULT 6

ID ADT1_RAT STANDARD; PRT; 298 AA.
 AC Q05962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.,
 RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.",
 RL Biochem. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----

CC EMBL; X61667; CA43842.1; -;
 CC EMBL; D12770; BAA02237.1; -;
 CC PIR; I60173; I60173.
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUOCOUPLING.
 DR PROSITE; PS00215; MITOCH CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6B320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1e-117;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISKTAVPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60
 DB 1 MGDQALSLKDFLAGGIAAISKTAVPIERVKLLQVQHASKQISAKQYKGIIDCVR 60
 QY 61 IPKEGQVSPFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVHGTQFMRFFAGNLSG 120
 DB 61 IPKEGQVSPFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVHGTQFMRFFAGNLSG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLVKITKSDIGRLYGQFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLVKITKSDIGRLYGQFSVS 180
 QY 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIVSWMIAQTVAAGVSYPPDYRRRRMM 240
 DB 181 VGGIITRYAAYFGVYDTAKGMLPDPKNTHTIFISWMIAGSVTAAGLTSYPPDYRRRRMM 240
 QY 241 QSGRGADIMTGTGVDCKRKIFRDEGKAFKFGKANSNVLKMGCAFVLVYDELKVI 298
 DB 241 QSGRGADIMTGTGVDCKRKIFRDEGKAFKFGKANSNVLKMGCAFVLVYDELKVI 298

RESULT 7

ID ADT1_MOUSE STANDARD; PRT; 298 AA.
 AC P48962; O62164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1) (MAMC1).
 GN SLC25A4 OR ANT1 OR ANCL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
  homologs.";
RL Mamm. Genome 7:25-30 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
  translocase 1 and 2 genes.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
  Brownstein M.J., Umed T.B., Toshyuki S., Carrinci P., Prange C.,
  Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
  Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
  Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
  human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
  MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
  inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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  entities requires a license agreement (See http://www.ebi.ac.uk/announcements
  or send an email to license@ebi.ac.uk.)
CC -----
DR EMBL: U27315; AAC52837.1; -
DR EMBL: X74510; CA52616.1; -
DR EMBL: AF240002; AAF64470.1; -
DR EMBL: BC003791; AAH03791.1; -
DR EMBL: BC026925; AAH26925.1; -
DR PIR: S37210; S37210.
DR MGD: MGI:1353495; S1C25A4.
DR InterPro: IPR002067; Mit carrier.
DR InterPro: IPR002030; Mit uncoupling.
DR InterPro: IPR001993; Mitoch carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.

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KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT REPEAT 136 136 F -> L (IN REF. 1).
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEB0981462 CRC64;

Query Match 91.9%; Score 1418; DB 1; Length 298;
Best Local Similarity 86.9%; Pred. No. 3.4e-117;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQATSPANDFLAGGIAAISKTAAPLIERVLLQVQHASKOIADKQYKIVDCIVR 60
DB 1 MGQALSLFKDPLAGGIAAASKTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVR 60
QY 61 IPKEQVLSFRWGNLANVIRYPTQALNFAFKKQKQIFGVYDKTQFWRYPAGNLASG 120
DB 61 IPKEQGLSFRWGNLANVIRYPTQALNFAFKKQKQIFGVYDKTQFWRYPAGNLASG 120
QY 121 GAAGATSLCPVPLDPARTLADVQSGTEREFGDGLVYKTSDDGIRGLYOGFSVS 180
DB 121 GAAGATSLCPVPLDPARTLADVQSGTEREFGDGLVYKTSDDGIRGLYOGFSVS 180
QY 181 VQGIIRYRAAFGVYDTAKMLPDPKNTHTIVSMIAQTVTAAGVSYDPDTRRRMM 240
DB 181 VQGIIRYRAAFGVYDTAKMLPDPKNTHTIVSMIAQTVTAAGVSYDPDTRRRMM 240
QY 241 QSGRKADIVYTGTDGWRKIFPDDEGKAFPKGAMSVTLFGMGAFVLYLYDELKXY 298
DB 241 QSGRKADIVYTGTDGWRKIFPDDEGKAFPKGAMSVTLFGMGAFVLYLYDELKXY 298

RESULT 8
ADTI_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
  differences in various tissues.";
RL Biochemistry 28:866-873 (1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Mista D., Bultz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
  mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349 (1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

```


RT an unusually short 3'-noncoding sequence.";
 RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M13783; AAA0363.1; -;
 DR EMBL; M24102; AAA0768.1; -;
 DR PIR; A43646; XMBO.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_catr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family; Methylation.
 FT INIT_MET 0
 FT MOD_RES 1 1 BLOCKED.
 FT MOD_RES 51 51 METHYLATION (POTENTIAL).
 FT TRANSSEM 11 28 1 (POTENTIAL).
 FT TRANSSEM 72 90 2 (POTENTIAL).
 FT TRANSSEM 116 133 3 (POTENTIAL).
 FT TRANSSEM 175 194 4 (POTENTIAL).
 FT TRANSSEM 213 230 5 (POTENTIAL).
 FT TRANSSEM 272 290 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 207 2.
 FT REPEAT 208 297 3.
 SQ SEQUENCE 297 AA; 32836 MW; A582D3CA4A0EB48 CRC64;
 Query March 91.8%; Score 1417; DB 1; Length 297;
 Best Local Similarity 89.2%; Pred. No. 4.1e-117;
 Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
 QY 2 TEQAIISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKQIAADKQYGIYDCIVRI 61
 DB 1 SDQALSFIDKPLAGVAIAISKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRI 60
 QY 62 PKEGVTSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDYDHTQFWRYPAGNLASGG 121
 DB 61 PKEGVTSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDYDHTQFWRYPAGNLASGG 120
 QY 122 AAGATSLCFVYPLDFAFRLADVGKSTEREFGDGLVITKISGIRGLYGFVSIV 181
 DB 121 AAGATSLCFVYPLDFAFRLADVGKGAQREFTGLNGCTIKRISGIRGLYGFVSIV 180
 QY 182 QGIIIVAAVFGVYDTAKGMLDPDKNTIIVSNMIAQTVTVAVAGVSPFPTVRRMMQ 241
 DB 181 QGIIIVAAVFGVYDTAKGMLDPDKNTIIVSNMIAQTVTVAVAGVSPFPTVRRMMQ 240
 QY 242 SGRKADIMVTGYDCKRKIFRDGGGAFFKGAANSVLRGNGAFVLVLYDELKVI 298
 DB 241 SGRKADIMVTGYDCKRKIAKDEGPRFAFFKGAANSVLRGNGAFVLVLYDEIKFV 297
 RESULT 9
 ADTI_HUMAN
 ID ADTI_HUMAN STANDARD; PRT; 298 AA.
 AC P12235;

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequence of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons,
 RT is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13998-14004(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041149; PubMed=2823266;
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,
 RT and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Eye;
 MEDLINE=22388257; PubMed=1247792;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.A., Halef F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Murthy M.C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.V., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallalath D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Touchman A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA "Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PRO PRO-114 AND MET-289.
 RX MEDLINE=20385067; PubMed=10926541;
 RA Kaukonen U., Jusselius J.K., Titiati V., Kyttala A., Zeviani M.,
 RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svraksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."; Science 287:2185-2195 (2000).
 RL
 RN
 RP
 RC STRAIN=Berkelley; TISSUE=Larva, Ovary, and Pupae;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guatrin H., Krommiller B., Paclebo J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celisner S.E.;
 RT "A *Drosophila* full-length cDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6(2002).
 CC
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- DOMAIN: Composed of three homologous domains.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; S43651; AAB23114.1; -;
 CC EMBL; S71762; AAB31734.3; -;
 CC EMBL; Y10618; CA971628.1; -;
 CC EMBL; AE003484; AAF47957.1; -;
 CC EMBL; AY060978; AAL48526.1; -;
 CC EMBL; AY070894; AAL48526.1; -;
 CC FlyBase; FBgn0003360; seeb.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0006839; P:mitochondrial transport; IMP.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR001993; Mltch_carrier.
 DR Pfam; PF00153; mltc_carrier; 2.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 215 232 5 (POTENTIAL).
 FT TRANSMEM 274 292 6 (POTENTIAL).
 FT TRANSMEM 18 19 G -> QV (IN REF. 1 AND 2).
 FT TRANSMEM 81 81 I -> Y (IN REF. 1).
 FT TRANSMEM 201 201 MISSING (IN REF. 1 AND 2).
 FT TRANSMEM 267 267 G -> A (IN REF. 2).
 FT TRANSMEM 268 269 TG -> P (IN REF. 1 AND 2).
 FT TRANSMEM 270 270 A -> S (IN REF. 2).
 FT TRANSMEM 270 270 A -> C (IN REF. 2).
 FT TRANSMEM 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;
 FT SEQUENCE

Query Match 81.3%; Score 1254.5; DB 1; Length 299;
 Best Local Similarity 80.6%; Pred. No. 7.5e-103;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 QY 5 AISPADKTLAAGIAAIAIKTAVAPIERVKLLQVHASKQIADKQYGVDCIPIKE 64
 DB 7 AVGFQKDAAGISAAVSKTAVAPIERVKLLQVHASKQIADKQYGVDCIPIKE 66
 QY 65 OGVSFWGNLANVRYPTALNFAFDKKQKQIFLGVDNHTQWRPFAGNLASGGAAG 124
 DB 67 OGFSFWGNLANVRYPTALNFAFDKKQKQIFLGVDNHTQWRPFAGNLASGGAAG 126
 QY 125 ATSLCFVPLDFARTRLAADVGSGTEREFGDCLVKITKSDIRGLYGSFVSVOGI 184
 DB 127 ATSLCFVPLDFARTRLAADVGSGS-QREFTGLGNCILKIKSDI VGLYGFVSVOGI 185
 QY 185 IYRAAYGVYDTAKMLPDPKNTIIVSMIAQTVTAAGVSYPTVRRMMQSGR 244
 DB 186 IYRAAYGVYDTAKMLPDPKNTIIVSMIAQTVTAAGVSYPTVRRMMQSGR 245
 QY 245 KGADIMYGVYDQWRKIIRDEGGAFFKGASNTLRGCAFVLYLDELKVI 298
 DB 246 KATEVINYNTLHCWATIAKQEGTGAFKGAFTNLRGTGAFVLYLDELKVI 299
 RESULT 11
 ADT_ANOGA
 ID ADT_ANOGA STANDARD; PRT; 301 AA.
 AC Q27238;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 DE translocator) (ANT).
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G3;
 RX MEDLINE=94348635; PubMed=8069414;
 RA Beard C.B., Crews-Oyen A.B., Kumar V.K., Collins F.H.;
 RT "A cDNA encoding an ADP/ATP carrier from the mosquito *Anopheles*
 RT *gambiae*."; Insect Mol. Biol. 3:35-40(1994).
 RL
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L11618; AAB04104.1; -;
 CC EMBL; L11617; AAB04105.1; -;
 CC InterPro; IPR002067; Mlt_carrier.
 CC InterPro; IPR001993; Mltch_carrier.
 CC Pfam; PF00153; mltc_carrier; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM

Query Match 78.0%; Score 1204; DB 1; Length 301;
Best Local Similarity 77.7%; Pred. No. 2,1e-98;
Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 216 233 5 (POTENTIAL).
FT TRANSMEM 275 293 6 (POTENTIAL).
SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;
Best Local Similarity 77.7%; Pred. No. 2,1e-98;
Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

1 MTEQA--ISFAKDLAGGIAAISKTAVERKLLQVQHASKQIADKQYGIYDCI 58
1 MTKADADYGAFAKPLAGGISAASVKTAVAPLBRKLLQVQASQIADKQYGIYDCI 60

59 VRIPEKGGVAFWFGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQFWRYPAGNLA 118
61 VRIPEKGGVAFWFGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQFWRYPAGNLA 120

119 SGGAAGATSLCFVYPLDFAFRLADVAGSGTEREFGDGLVKTSGDGRGLYOGFS 178
121 SGGAAGATSLCFVYPLDFAFRLADVAGSGTEREFGDGLVKTSGDGRGLYOGFS 180

179 VSVGGIITVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQVTVAAGVSYPTVRRMM 238
181 VSVGGIITVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQVTVAAGVSYPTVRRMM 240

239 MMOSGRKADIMYGTVDCKWRKIFRDEGKAFFKGAWSNVLRGGAFAVLVYDELKVI 298
241 MMOSMPCKSEVMYNTIDCWVKIKQKSGSAGFAFGASNVLRGGLVLFVDEVAL 300

RESULT 12
ADT_CHLKE STANDARD; PRT; 339 AA.

AC P1692;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryote; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.
ON NCBI_TaxID=3074;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=92084708; PubMed=1748677;
RA Hilgatch C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC EMBL; M76669; AAA33027.1; -
CC PIR; A41677; A41677;
DR InterPro: IPR002067; Mit_carrier
DR InterPro: IPR001993; Mitoch_carrier
DR Pfam; PF00153; mito_carr; 3
DR PRINTS; PR00926; MITOCHARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.

Query Match 63.4%; Score 978; DB 1; Length 339;
Best Local Similarity 66.9%; Pred. No. 1.6e-78;
Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 45 62 1 (POTENTIAL).
FT TRANSMEM 108 126 2 (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT TRANSMEM 209 228 4 (POTENTIAL).
FT TRANSMEM 248 265 5 (POTENTIAL).
FT TRANSMEM 304 322 6 (POTENTIAL).
SQ SEQUENCE 339 AA; 36866 MW; 54779734A3B3942 CRC64;

6 ISFAKDLAGGIAAISKTAVERKLLQVQHASKQIADKQYGIYDCI 63
39 MAFVKKDLAGGIAAISKTAVERKLLQVQHASKQIADKQYGIYDCI 98

64 EGVLSFWRGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQFWRYPAGNLA 123
99 EGVLSFWRGNLANVIRYPTQALNFAFKDKYQIPLGVDKHTQFWRYPAGNLA 157

124 GATSLCFVYPLDFAFRLADVAGSGTEREFGDGLVKTSGDGRGLYOGFSVVOG 183
158 GATSLCFVYPLDFAFRLADVAGSGTEREFGDGLVKTSGDGRGLYOGFSVVOG 216

184 IIVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQVTVAAGVSYPTVRRMM 242
217 IIVRAAYGVYDTAKGMLPDPKNTIIVSMMIAQVTVAAGVSYPTVRRMM 276

243 GRRGADIMYGTVDCKWRKIFRDEGKAFFKGAWSNVLRGGAFAVLVYDELKVI 298
277 GRRGADIMYGTVDCKWRKIFRDEGKAFFKGAWSNVLRGGAFAVLVYDELKVI 329

RESULT 13
ADT_YEAST STANDARD; PRT; 307 AA.

AC P18238;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).
GN AAC3 OR YBR085W OR YBR0753.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomycaceae.
ON NCBI_TaxID=4932;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=90324269; PubMed=2165073;
RA Kolacov J., Kolacova N., Nelson N.;
RT "A third ADP/ATP translocator gene in yeast.";
RL J. Biol. Chem. 265:12711-12716(1990).
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=S288C;
CC Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
CC Vissers S.;
CC Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC [3]
CC SEQUENCE OF 38-307 FROM N.A.
CC STRAIN=S288C;
CC Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
CC Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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EMBL: M34076; AAA97485.1; -
 DR EMBL: Z35954; CAA85031.1; -
 DR PIR: A36582; A36582.
 DR SCD: S0000289; AAC3.
 DR GO: GO:0005471; F:ATP/ADP antiporter activity; IMP.
 DR GO: GO:0006854; P:ATP/ADP exchange; IMP.
 DR InterPro: IPR002067; Mito_carrier.
 DR InterPro: IPR001993; MitoCh_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCHARRIER.
 DR PROSITE: PS00215; MITOCH CARRIER; 2.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 16 33 1 (POTENTIAL).
 FT TRANSMEM 78 96 2 (POTENTIAL).
 FT TRANSMEM 120 137 3 (POTENTIAL).
 FT TRANSMEM 181 200 4 (POTENTIAL).
 FT TRANSMEM 220 237 5 (POTENTIAL).
 FT TRANSMEM 276 294 6 (POTENTIAL).
 FT TRANSMEM 307 AA; 33313 MW; DC1329FEC1BADC8 CRC64;
 SQ SEQUENCE 307 AA; 33313 MW; DC1329FEC1BADC8 CRC64;

Query Match 50.5%; Score 778.5; DB 1; Length 307;
 Best Local Similarity 53.7%; Pred. No. 4.5e-61;
 Matches 161; Conservative 45; Mismatches 85; Indels 9; Gaps 5;

QY 3 EQATSPADFLAGIAAISTAVAPIERVKLLQVQ-HASQIADAKQYKIVDCIRI 61
 Db 7 QOETNFALNFMGVSAAIATAPIERVKILLIONOEMIKQGLDKKYGIVDCIFKRT 66
 QY 62 PKEOGVLSFMRGNLANVRYEPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASGG 121
 Db 67 AKQEGSLFMRGNLANVRYEPTQALNFAFKDKITLM--GFKKEGSGKMFAGNLASGG 124
 QY 122 AAGATSLCFVYPLDFARTRLADV--GKSGTEREFGIGDCLVKITKSDGIRGLYQGFVS 179
 Db 125 AAGALSLFVYSLDFARTRLADAKSKKGGARQFNGLTQYKTLKSDGIAGLYGRFMP 184
 QY 180 SVQGIITIRAAVFGVYDTAKGM-LPDPKNTIIVSMIAQVTVTAAGVVSYPFDTVR 238
 Db 185 SVGIIVYRGVYFGVYDTAKGM-LPDPKNTIIVSMIAQVTVTAAGVVSYPFDTVR 244
 QY 239 MMOSGRKADIMYGTVDQWKRIFRDEGGKAFKFGKANSNVLRMGGAFLVLYDELKVI 298
 Db 245 MMTSGQA--VKYNGAIDCLKKIIVASBEVGSLEFKGCGANILRSVAGAVISMTDQLQMTL 301

RESULT 14
 ADT_CHLRE STANDARD; PRT; 308 AA.
 ID ADT_CHLRE P2780.
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANT.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUD44-R2;
 RX MEDLINE=93204887; PubMed=8455552;
 RA Sharpe J.A., Day A.;

"Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.";
 RL Mol. Gen. Genet. 237:134-144(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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EMBL: X65194; CAA46311.1; -
 DR PIR: G30259; S30259.
 DR InterPro: IPR002067; Mito_carrier.
 DR InterPro: IPR001993; MitoCh_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCHARRIER.
 DR PROSITE: PS00215; MITOCH CARRIER; 2.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 74 92 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 217 234 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT TRANSMEM 308 AA; 33528 MW; D477CF0E72B7A53P CRC64;
 SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53P CRC64;

Query Match 50.0%; Score 772; DB 1; Length 308;
 Best Local Similarity 51.8%; Pred. No. 1.7e-60;
 Matches 157; Conservative 55; Mismatches 81; Indels 10; Gaps 5;

QY 1 MTEQATSPADFLAGIAAISTAVAPIERVKLLQVQ-HASQIADAKQYKIVDCIRI 59
 Db 1 MAKEKQFMVDFLAGGSAVASKTAAPIERVKILLIONOEMIKQGLASPYKIGICEFV 60
 QY 60 RPKEOGVLSFMRGNLANVRYEPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAS 119
 Db 61 RTVEBEGSLMRGNLANVRYEPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAS 118
 QY 120 GGAAGATSLCFVYPLDFARTRLAD--VGKSGTEREFGIGDCLVKITKSDGIRGLYQ 176
 Db 119 GGAAGATSLCFVYPLDFARTRLADAKSAGKGGDROFNGLVYRKTIASDGIAGLYRG 178
 QY 177 FSVSVGGIITIRAAVFGVYDTAKG-MLPDPKNTIIVSMIAQVTVTAAGVVSYPFDTVR 235
 Db 179 FNISCVGIIVYRGVYFGVYDTAKG-MLPDPKNTIIVSMIAQVTVTAAGVVSYPFDTVR 238
 QY 236 RMMOSGRKADIMYGTVDQWKRIFRDEGGKAFKFGKANSNVLRMGGAFLVLYDELKVI 295
 Db 239 RRMNMTS--GSAAVKNSSPHCFQELVKNKMSLFRGAGANILRSVAGAVISMTDQLQMTL 295
 QY 296 KVI 298
 Db 296 VIL 298

RESULT 15
 ADT_SCHPO STANDARD; PRT; 322 AA.
 ID ADT_SCHPO O09188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN translocator (ANT).
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUD44-R2;
 RX MEDLINE=93204887; PubMed=8455552;
 RA Sharpe J.A., Day A.;

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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 20 Seconds

(without alignments)
1432.913 Million cell updates/sec

Title: US-09-185-904A-33

Perfect score: 1543
Sequence: 1 MTEQALSFADFLAGLAI...LRMGAFVLVYDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1 S03894	ADP,ATP carrier pr
2	1512	98.0	298	2 B43646	ADP,ATP carrier pr
3	1454	94.2	298	1 A29132	ADP,ATP carrier pr
4	1424	92.3	298	1 I60173	adenine nucleotide
5	1422	92.2	298	1 XWBO	ADP,ATP carrier pr
6	1418	91.9	298	2 S37210	ADP,ATP carrier pr
7	1409	91.3	298	1 A44778	ADP,ATP carrier pr
8	1405	91.1	298	2 S31814	ADP,ATP carrier pr
9	1184	76.7	301	1 S31935	ADP,ATP carrier pr
10	1041	67.5	313	2 T23207	ADP,ATP carrier pr
11	1039	67.3	313	1 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP,ATP carrier pr
15	943	61.1	301	2 S51132	ADP,ATP carrier pr
16	778.5	50.0	307	2 A36582	ADP,ATP carrier pr
17	772	50.5	308	1 S30259	ADP,ATP carrier pr
18	769	49.8	322	2 T40526	ADP,ATP translocas
19	768	49.8	386	2 T09709	ADP,ATP carrier pr
20	766	49.6	313	1 XWNC	ADP,ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP,ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP,ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14876	ADP,ATP carrier pr
26	748	48.5	386	2 S21974	ADP,ATP carrier pr
27	747	48.4	306	2 T42011	ADP,ATP carrier pr
28	747	48.4	386	2 S17917	ADP,ATP carrier pr
29	744	48.2	387	2 S16568	ADP,ATP carrier pr

30	743	48.2	379	2 T04608	ADP,ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP,ATP carrier pr
32	742	48.1	382	2 S33630	ADP,ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP,ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP,ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP,ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP/ATP translocas
38	383	24.8	325	2 T01273	hypothetical prote
39	381	24.7	352	2 T01729	mitochondrial solu
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	363	23.5	348	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

S03894
ADP,ATP carrier protein T3 - human
N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,ATP
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: S03894; B28116
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03854
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Houldsworth, J.; Attardi, G.
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A:Reference number: A94197; MUID:86124845; PMID:2829183
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HO>
A:Reference number: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT3; ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: XP22.32-XP22.33; Yp11.3-Yp11.3
A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domin: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domin: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domin: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best local similarity 100.0%; Pred. No. 6e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTEQALSFADFLAGLAIISKTAVPRIKVLLOVHASQIADKQYGVDCIVR	60
Db	1	MTEQALSFADFLAGLAIISKTAVPRIKVLLOVHASQIADKQYGVDCIVR	60
Qy	61	IPKEQGLSFWRGUINAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFRYFAGNLASG	120
Db	61	IPKEQGLSFWRGUINAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFRYFAGNLASG	120
Qy	121	GAAGATSLCFVYPIIDFARTRLADVKGSGTEREERFGIDCLVITKYSQDGIKGLYOGFSVS	180
Db	121	GAAGATSLCFVYPIIDFARTRLADVKGSGTEREERFGIDCLVITKYSQDGIKGLYOGFSVS	180

QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQOTVAAGVSYFEDTVRRMM 240
 |||||
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQOTVAAGVSYFEDTVRRMM 240
 |||||
 QY 241 QSGRKADIMVTGTVDKWKIFRDEGGKAFPGKAMSVNLKMGCAFVLVYDELKVI 298
 |||||
 DB 241 QSGRKADIMVTGTVDKWKIFRDEGGKAFPGKAMSVNLKMGCAFVLVYDELKVI 298
 |||||

RESULT 2

B43646
 ADP/ATP carrier protein T2 - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C/Accession: B43646
 R/Powell, S.U.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A/Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A/Reference number: A43646; MUID:89229093; PMID:2540808
 A/Accession: B43646
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-298 <POM>
 A/Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 3,3e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISFADPLAGGIAAISTKTAAPIERVKLLQVQHASQIADKQYKGIIDCIVR 60
 |||||
 DB 1 MTEQAISFADPLAGGIAAISTKTAAPIERVKLLQVQHASQIADKQYKGIIDCIVR 60
 |||||
 QY 61 IPEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 |||||
 DB 61 IPEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 |||||
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKSGEREERFGDCLVKITKSDGIRGLYQGFVS 180
 |||||
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKSGEREERFGDCLVKITKSDGIRGLYQGFVS 180
 |||||
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQOTVAAGVSYFEDTVRRMM 240
 |||||
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQOTVAAGVSYFEDTVRRMM 240
 |||||
 QY 241 QSGRKADIMVTGTVDKWKIFRDEGGKAFPGKAMSVNLKMGCAFVLVYDELKVI 298
 |||||
 DB 241 QSGRKADIMVTGTVDKWKIFRDEGGKAFPGKAMSVNLKMGCAFVLVYDELKVI 298
 |||||

RESULT 3

A29132
 ADP/ATP carrier protein T2 - human
 N/Alternate names: mitochondrial ADP/ATP translocase 2
 C/Species: Homo sapiens (man)
 C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C/Accession: A29132; C26116
 R/Bertini, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 267, 4355-4359, 1987
 A/Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A/Reference number: A29132; MUID:8716056; PMID:3031073
 A/Accession: A29132
 A/Molecule type: mRNA
 A/Residues: 1-298 <BAT>
 A/Cross-references: GB:002663; NID:9179246; PIDN:AAA35579.1; PID:9179247
 R/Houldsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A/Reference number: A94197; MUID:88124845; PMID:2829183
 A/Accession: C28116
 A/Molecule type: mRNA
 A/Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A/Cross-references: GB:003591; NID:9339720; PIDN:AAA36749.1; PID:9339721
 A/Experimental source: clone PHAT3
 C/Genetics:
 A/Genes: GDB:ANT2; T3; 2P1
 A/Cross-references: GDB:125190; OMIM:300150
 A/Map position: Xq13-Xq26
 A/Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:1

C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 4.5e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFADPLAGGIAAISTKTAAPIERVKLLQVQHASQIADKQYKGIIDCIVR 60
 |||||
 DB 1 MTEQAISFADPLAGGIAAISTKTAAPIERVKLLQVQHASQIADKQYKGIIDCIVR 60
 |||||
 QY 61 IPEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 |||||
 DB 61 IPEQGVLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 |||||
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKSGEREERFGDCLVKITKSDGIRGLYQGFVS 180
 |||||
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKSGEREERFGDCLVKITKSDGIRGLYQGFVS 180
 |||||
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQOTVAAGVSYFEDTVRRMM 240
 |||||
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQOTVAAGVSYFEDTVRRMM 240
 |||||
 QY 241 QSGRKADIMVTGTVDKWKIFRDEGGKAFPGKAMSVNLKMGCAFVLVYDELKVI 296
 |||||
 DB 241 QSGRKADIMVTGTVDKWKIFRDEGGKAFPGKAMSVNLKMGCAFVLVYDELKVI 296
 |||||

RESULT 4

160173
 adenine nucleotide translocator - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C/Accession: 160173
 R/Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A/Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat n
 A/Reference number: 160173; MUID:94002161; PMID:8399300
 A/Accession: 160173
 A/Status: preliminary; translated from GB/EMBL/DDJ
 A/Molecule type: DNA
 A/Residues: 1-298 <RES>
 A/Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427
 C/Genetics:
 A/Genes: anti1
 A/Intons: 37/3; 200/1; 247/1
 C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C/Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFADPLAGGIAAISTKTAAPIERVKLLQVQHASQIADKQYKGIIDCIVR 60
 |||||
 DB 1 MTEQAISFADPLAGGIAAISTKTAAPIERVKLLQVQHASQIADKQYKGIIDCIVR 60
 |||||

QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVGSCTERBERGDLGVKTKSGDITGLYOGFSVS 180
 Db 121 GAAAGTSLCFYVPLDPFARTRLAADVGSCTERBERGDLGVKTKSGDITGLYOGFSVS 180
 QY 181 VGGIITRYAAFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSVSPFTVRRMM 240
 Db 181 VGGIITRYAAFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSVSPFTVRRMM 240
 QY 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRMGGAFLVLYDELKVI 298
 Db 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRMGGAFLVLYDELKVI 298

RESULT 5

XMB0
 ADP,ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M4102; NID:9529414; PIDN:AAA30768.1; PID:9529415
 R:Rasmussen, U.B.; Wohlrab, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:86295775; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <BAS>
 A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Mistr, D.; Bullitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: Protein
 A:Residues: 2-51, 'X', '53-70, 'X', '72-109, 'X', '111-298 <AGU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Machter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oertmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63,154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochond
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;

Best Local Similarity 89.3%; Pred. No.3,1e-118; Mismatches 13; Indels 0; Gaps 0;

Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQALISPAKDFLAGGIAAISKTAVAIEFEVKLLQVQHASKOIADKOYKGIIDCV 60
 Db 1 MSDQALSLKDFLAGGVAIAISKTAVAIEFEVKLLQVQHASKOIADKOYKGIIDCV 60
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVGSCTERBERGDLGVKTKSGDITGLYOGFSVS 180
 Db 121 GAAAGTSLCFYVPLDPFARTRLAADVGSCTERBERGDLGVKTKSGDITGLYOGFSVS 180
 QY 181 VGGIITRYAAFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSVSPFTVRRMM 240
 Db 181 VGGIITRYAAFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSVSPFTVRRMM 240
 QY 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRMGGAFLVLYDELKVI 298
 Db 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRMGGAFLVLYDELKVI 298

RESULT 6

ADP,ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Laplace, C.; Coetzel, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <LAP>
 A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
 C:Genetics:
 A:Gene: ANCI
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.9%; Score 1418; DB 2; Length 298;

Best Local Similarity 88.9%; Pred. No.6,9e-118; Mismatches 14; Indels 0; Gaps 0;

Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQALISPAKDFLAGGIAAISKTAVAIEFEVKLLQVQHASKOIADKOYKGIIDCV 60
 Db 1 MGDQALSLKDFLAGGIAAISKTAVAIEFEVKLLQVQHASKOIADKOYKGIIDCV 60
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVGSCTERBERGDLGVKTKSGDITGLYOGFSVS 180
 Db 121 GAAAGTSLCFYVPLDPFARTRLAADVGSCTERBERGDLGVKTKSGDITGLYOGFSVS 180
 QY 181 VGGIITRYAAFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSVSPFTVRRMM 240
 Db 181 VGGIITRYAAFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSVSPFTVRRMM 240
 QY 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRMGGAFLVLYDELKVI 298
 Db 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRMGGAFLVLYDELKVI 298

Db 241 QSGRKGADIMVTGTLDCWKRKIADEGANAFKGMASVLRGMGAFVLVLYDEIKKYV 298

RESULT 7

A44778
ADP, ATP carrier protein T1 - human
N/Alternate names: mitochondrial ADP, ATP translocase 1
C/Species: Homo sapiens (man)
C/Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000
C/Accession: A44778; S03893; A39891; A28116
R/L1, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1989
A/Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A/Reference number: A44778; MUID:89340499; PMID:2547778
A/Accession: A44778
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-298 <LTA>
A/Cross-references: GB:U04982; NID:G178658; PIDN:AAA51736.1; PID:G178659
R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A/Reference number: S03893; MUID:89236396; PMID:2541251
A/Accession: S03893
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-298 <COZ>
R/Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A/Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader
A/Reference number: A39891; MUID:88041149; PMID:2823266
A/Accession: A39891
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A/Cross-references: GB:U02966; NID:G339919; PIDN:AAA61223.1; PID:G339920
A/Experimental source: clone pHMANT
R/Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A/Reference number: A94197; MUID:88124845; PMID:2829183
A/Accession: A28116
A/Molecule type: mRNA
A/Residues: 1-37 <HOU>
A/Cross-references: GB:J03593; NID:G339724; PIDN:AAA36751.1; PID:G339725
A/Experimental source: liver
A/Genetics:
A/Gene: GDB:ANT1; T1
A/Cross-references: GDB:119680; OMIM:103220
A/Map position: 4q35-4q35
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: duplication, homodimer; mitochondrion; transmembrane protein
F/2-298/Product: ADP, ATP carrier protein #status predicted <MAT>
F/5-99/Domains: ADP, ATP carrier protein repeat homology <ACP1>
F/110-202/Domains: ADP, ATP carrier protein repeat homology <ACP2>
F/207-298/Domains: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;
Best Local Similarity 88.3%; Pred. No. 4.3e-117;
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQAI SPADFLAGI AAIISKTA VAPIERVKLLQVQHASKOIADKQYKGI VDCIVR 60
Db 1 MGHIAVFLDPLAGVAAAVSKTA VAPIERVKLLQVQHASKOIASEKQYKGIIDCVR 60
QY 61 IPKEQGLSFWRGKLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGKLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSKDGIRGLYQGFVS 180
Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSKDGIRGLYQGFVS 180
121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSKDGIRGLYQGFVS 180

QY 181 VQGIITRYAAYFGVYDTAKGMLPDPKNTIHVSWMTAQVTA VAGVSVYFDTVRRMM 240
Db 181 VQGIITRYAAYFGVYDTAKGMLPDPKNTIHVSWMTAQVTA VAGVSVYFDTVRRMM 240

QY 241 QSGRKGADIMVTGTVDCWKRKIFDEGKAFFKGMASVLRGMGAFVLVLYDEIKKYV 298
Db 241 QSGRKGADIMVTGTVDCWKRKIADEGANAFKGMASVLRGMGAFVLVLYDEIKKYV 298

RESULT 8

S31814
ADP, ATP carrier protein T2 - mouse
N/Alternate names: adenine nucleotide translocase
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 09-Apr-1998
C/Accession: S31814
R/Costel, P.; Lapiere, C.
submitted to the EMBL Data Library, January 1993
A/Reference number: S31814
A/Accession: S31814
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-298 <COS>
A/Cross-references: EMBL:X70847
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: duplication, transmembrane protein
F/5-99/Domains: ADP, ATP carrier protein repeat homology <ACP1>
F/110-202/Domains: ADP, ATP carrier protein repeat homology <ACP2>
F/207-298/Domains: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;
Best Local Similarity 89.2%; Pred. No. 9.8e-117;
Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQAI SPADFLAGI AAIISKTA VAPIERVKLLQVQHASKOIADKQYKGI VDCIVR 60
Db 1 MTEQAI SPADFLAGI AAIISKTA VAPIERVKLLQVQHASKOIADKQYKGI VDCIVR 60

QY 61 IPKEQGLSFWRGKLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
Db 61 IPKEQGLSFWRGKLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSKDGIRGLYQGFVS 180
Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSKDGIRGLYQGFVS 180

QY 181 VQGIITRYAAYFGVYDTAKGMLPDPKNTIHVSWMTAQVTA VAGVSVYFDTVRRMM 240
Db 181 VQGIITRYAAYFGVYDTAKGMLPDPKNTIHVSWMTAQVTA VAGVSVYFDTVRRMM 240

QY 241 QSGRKGADIMVTGTVDCWKRKIFDEGKAFFKGMASVLRGMGAFVLVLYDEIKKYV 298
Db 241 QSGRKGADIMVTGTVDCWKRKIADEGANAFKGMASVLRGMGAFVLVLYDEIKKYV 298

RESULT 9

S31935
ADP, ATP carrier protein - African malaria mosquito
C/Species: Anopheles gambiae (African malaria mosquito)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S31935; S31936
R/Beard, C.B.; Crews-Owen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A/Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.
A/Reference number: S31935
A/Accession: S31935
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-301 <BEA>
A/Cross-references: EMBL:Z21814; EMBL:Z21815
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: duplication, transmembrane protein
F/7-101/Domains: ADP, ATP carrier protein repeat homology <ACP1>

F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 76.7%; Score 1184; DB 1; Length 301;
Best Local Similarity 77.0%; Pred. No. 3.6e-97;
Matches 231; Conservative 23; Mismatches 44; Indels 2; Gaps 1;

QY 1 MTEQA-15FAKDFLAGIAAISTKAVAPIERVKLLQVQHASQIADKQYKIVDCI 58
DB 1 MTKKADPYGPAKDFLAGGISAASVSTAVAPIERVKLLQVQHASQIADKQYKIVDCI 60
QY 59 VRIPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFGVGDKHTQFMRYPAGNLA 118
DB 61 VRIPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFGVGDKHTQFMRYPAGNLA 120
QY 119 SGGAAGATSLCFVYPLDFAFRTLLADVGKSGTEREFGGLDCLVYKTSDDGIRGLYQSGS 178
DB 121 SGGAAGATSLCFVYPLDFAFRTLLADVGKSGTEREFGGLDCLVYKTSDDGIRGLYQSGS 180
QY 179 VSVQGIITVRAAYFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRM 238
DB 181 VSVQGIITVRAAYFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRM 240
QY 239 MMQSGRKADIMVTGTVDCKWRIKFRDEGKAFFKGAWSNVLRMGGAFLVLYDELKRYI 298
DB 241 MMQSGRKSEVMYKNTLDCWVKIKQEGSGAFAFKGAFSNVLRMGGAFLVLYDEVKALL 300

RESULT 10

T23207
hypochemical protein K01H12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207

R:McMurray, A.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z19707

A:Accession: T23207

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <Wtl>

A:Cross-references: EMBL: Z68218; PIDN: CAA92472.1; GSPDB: GNO00022; CESP: K01H12.2

A:Experimental source: clone K01H12

C:Genetics:

A:Gene: CESP:K01H12.2

A:Map position: 4

A:Insertions: 4/1; 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.5%; Score 1041; DB 2; Length 313;
Best Local Similarity 70.9%; Pred. No. 1.7e-84;
Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDFLAGIAAISTKAVAPIERVKLLQVQHASQIADKQYKIVDCIIRPEKQGV 67
DB 25 FLIDLASGTAASVSTAVAPIERVKLLQVQDASLTIAADKRYGIVDVLRVPEKGY 84
QY 68 LSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 127
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 144
QY 128 LCFVYPLDFAFRTLLADVGKSGTEREFGGLDCLVYKTSDDGIRGLYQSGSVOGIIIT 187
DB 145 LCFVYPLDFAFRTLLADVGKSGTEREFGGLDCLVYKTSDDGIRGLYQSGSVOGIIIT 203
QY 188 RAAAFGVYDTAKGML-PDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRK 246
DB 204 RAAAFGVYDTAKGML-PDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRK- 262
QY 247 ADIMVTGTVDCKWRIKFRDEGKAFFKGAWSNVLRMGGAFLVLYDELKRYI 298
DB 263 -DVLYKNTLDCWVKIKQEGSGAFAFKGAFSNVLRMGGAFLVLYDEVKALL 313

RESULT 11
T25850
hypochemical protein T01B11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T25850

C:Status: C.; Steilly, L.

submitted to the EMBL Data Library, December 1996

A:Description: The sequence of C. elegans cosmid T01B11.

A:Reference number: Z20099

A:Accession: T25850

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <GRI>

A:Cross-references: EMBL: U80931; PIDN: AAB38001.1; GSPDB: GNO00022; CESP: T01B11.4

A:Experimental source: strain Bristol N2; clone T01B11

C:Genetics:

A:Gene: CESP:T01B11.4

A:Map position: 4

A:Insertions: 4/1; 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1039; DB 2; Length 313;
Best Local Similarity 70.9%; Pred. No. 2.6e-84;
Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDFLAGIAAISTKAVAPIERVKLLQVQHASQIADKQYKIVDCIIRPEKQGV 67
DB 25 FLIDLASGTAASVSTAVAPIERVKLLQVQDASLTIAADKRYGIVDVLRVPEKGY 84
QY 68 LSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 127
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 144
QY 128 LCFVYPLDFAFRTLLADVGKSGTEREFGGLDCLVYKTSDDGIRGLYQSGSVOGIIIT 187
DB 145 LCFVYPLDFAFRTLLADVGKSGTEREFGGLDCLVYKTSDDGIRGLYQSGSVOGIIIT 203
QY 188 RAAAFGVYDTAKGML-PDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRK 246
DB 204 RAAAFGVYDTAKGML-PDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRK- 262
QY 247 ADIMVTGTVDCKWRIKFRDEGKAFFKGAWSNVLRMGGAFLVLYDELKRYI 298
DB 263 -DVLYKNTLDCWVKIKQEGSGAFAFKGAFSNVLRMGGAFLVLYDEVKALL 313

RESULT 12

T25371
hypochemical protein T27B9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T25371

C:Status: C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z20024

A:Accession: T25371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <Wtl>

A:Cross-references: EMBL: Z82059; PIDN: CAB04874.1; GSPDB: GNO00021; CESP: T27B9.1

A:Experimental source: clone T27B9

C:Genetics:

A:Gene: CESP:T27B9.1

A:Map position: 3

A:Insertions: 20/1; 41/3; 115/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1038; DB 2; Length 300;
Best Local Similarity 69.2%; Pred. No. 3e-84;
Matches 202; Conservative 37; Mismatches 49; Indels 4; Gaps 3;

Db 8 NPAADFLMGISAIKTVVPIERVKMLIQTQDSIPEIKSGOVERYSGLINCERVSKE 67
 Qy 65 QGVLSFMRGNLANVIRYFPTQALNFAFKDKYQIFLAGVDKHTQFMRYFAGNLASGAAG 124
 Db 68 QGVLSMRGNVANVIRYFPTQALNFAFKDYKNIF-PRYDQNTDPSKEFCVNIISGATAG 126
 Qy 125 ATSLCEVYPLDPARTRLADVKGSGTEREFRLGDLVKITKSDGIRGLYOGFSVYOGI 184
 Db 127 AISLILIVYPLDPARTRLASDICK-GKDRQFTGLFDCLAKIYKQTGLSLYSGFVSVTGI 185
 Qy 185 IIRRAAFGVYDTAKML-PDBKNTIYVSMIAQYTAVAGVSYPPDYARRRMMOSG 243
 Db 186 IYRGSYFGLYDSAKALLFTNDKNTNIYIKWAVASVTILAGLISYPPDYARRRMMMSG 245
 Qy 244 RKG-ADIMYTGTVDCMRKIFRDEGGAFFKGAWSNVLRGMGAFVLYLDELKXVI 298
 Db 246 RKGKEIQYKNTIDCMIKILRNEGKGFPGKAMANVIRGAGALVLFYDELQKLI 301

Search completed: December 18, 2003, 17:11:23
 Job time : 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 / Search time 41 Seconds
(without alignments)
1875.602 Million cell updates/sec

Title: US-09-185-904A-33
Perfect score: 1543
Sequence: 1 MTEQALSFAPKDFLAGIAAA.....LRGNGAFVLVDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTREMBL_23.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacterioph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1474	95.5	298	13 Q8AYM3	Q8AYM3 gallus gall
2	1451	94.0	298	6 Q8SQH5	Q8SQH5 bos taurus
3	1446	93.7	298	13 Q8JH10	Q8JH10 brachydantio
4	1422	92.2	298	6 O46373	O46373 oryctolagus
5	1421	92.1	298	13 Q919M9	Q919M9 xenopus lae
6	1414	91.6	298	11 Q8BV19	Q8BV19 mus musculu
7	1409	91.3	298	13 Q9PRH1	Q9PRH1 rana rugosa
8	1406	91.1	298	13 Q9PRH2	Q9PRH2 rana rugosa
9	1402	90.9	299	5 Q95VX4	Q95VX4 ethiostictu
10	1300	84.3	317	13 Q91J36	Q91J36 rana sylvat
11	1259	81.6	317	5 Q8IRAO	Q8IRAO drosophila
12	1254.5	81.3	312	5 Q9NHWS	Q9NHWS lucilia cup
13	1235.5	80.1	300	5 Q9NHWS	Q9NHWS lucilia cup
14	1187.5	77.0	288	5 O44093	O44093 drosophila
15	1183.5	76.7	288	5 O44094	O44094 drosophila
16	1176.5	76.2	304	5 Q25129	Q25129 halocynthia

17	1159	75.1	254	11 Q8BK05	Q8BK05 mus musculu
18	1137.5	73.7	307	5 O62526	O62526 drosophila
19	1119	72.5	315	4 Q9H0C2	Q9H0C2 homo sapien
20	1041	67.5	313	5 Q21103	Q21103 caenorhabdi
21	1039	67.3	313	5 P91410	P91410 caenorhabdi
22	1038	67.3	300	5 O45865	O45865 caenorhabdi
23	1036.5	67.2	310	10 Q8H727	Q8H727 phycophor
24	996	64.5	309	5 Q97470	Q97470 dictyosteli
25	993.5	64.4	300	5 O01813	O01813 caenorhabdi
26	993	64.4	300	5 Q17407	Q17407 caenorhabdi
27	973.5	63.1	318	5 Q9B036	Q9B036 toxoplasma
28	947	61.4	307	5 Q81J34	Q81J34 plasmodium
29	946.5	61.3	307	8 Q9XM22	Q9XM22 ascaris suu
30	944	61.2	301	5 Q25692	Q25692 plasmodium
31	944	61.2	301	5 Q8MVR4	Q8MVR4 euptotes sp
32	943	61.1	301	5 Q26006	Q26006 plasmodium
33	936	60.7	305	5 Q8MVR7	Q8MVR7 nyctotherus
34	932	60.4	308	5 Q8MVR8	Q8MVR8 nyctotherus
35	924	59.9	306	5 Q8MVR5	Q8MVR5 nyctotherus
36	924	59.9	308	5 Q8MVR6	Q8MVR6 nyctotherus
37	827	53.6	170	6 Q9XS69	Q9XS69 sus scrofa
38	778.5	50.5	305	3 Q9P8M1	Q9P8M1 yarrowia li
39	767.5	49.7	302	3 Q8J0M2	Q8J0M2 yarrowia li
40	764	49.5	326	5 P91270	P91270 caenorhabdi
41	760	49.3	307	5 Q76286	Q76286 trypanosoma
42	759	49.2	303	3 Q74260	Q74260 candida par
43	756.5	49.0	305	5 Q18683	Q18683 caenorhabdi
44	753	48.8	307	5 Q26697	Q26697 trypanosoma
45	749	48.5	315	3 Q8J0U1	Q8J0U1 gaeananomy

ALIGNMENTS

RESULT 1
Q8AYM3 ID Q8AYM3 PRELIMINARY; PRT; 298 AA.
AC Q8AYM3:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ATP/ADP antiporter.
GN AVANT.
OS Gallus Gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
OX [1]
RP SEQUENCE FROM N.A.
RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
RL and ANT mRNA in chicken skeletal muscle.";
RL EMBL Letc. 9-0-012021.
DR EMBL; AB086866; BAC15533.1; -.
SQ SEQUENCE 298 AA; 32847 MW; 1174CC5BEC400A10D CRC64;

QY	Query Match	95.5%	Score 1474;	DB 13;	Length 298;
Db	Best Local Similarity	93.0%;	Pred. No. 2.5e-125;		
	Matches 277;	Conservative 14;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1	MTEQALSFAPKDFLAGIAAISKTAVPPIERVKLLLOVHASKOIADKQYGVDCIVR	60		
Db	1	MADDAISFLKDFLARGVAAISKTAVPPIERVKLLLOVHASKOIADKQYGVDCIVR	60		
QY	61	IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGGVDKHTQFRYFAGNLAAG	120		
Db	61	IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQVFLGGVDKHTQFRYFAGNLAAG	120		
QY	121	GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSDDGIRGLYQGFSSVS	180		
Db	121	GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSDDGIRGLYQGFSSVS	180		
	121	GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTYSDDGIRGLYQGFSSVS	180		

QY 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPFDTVRBRMM 240
 DB 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPFDTVRBRMM 240
 QY 241 QSGRKGADIMYGTGTCWKRIIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKXYI 298
 DB 241 QSGRKGADIMYGTGTCWKRIIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKXYI 298

RESULT 2

Q8SOH5 PRELIMINARY; PRT; 298 AA.
 ID Q8SOH5
 AC Q8SOH5;
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Adenine nucleotide translocator 2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
 RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
 RT "Identification of possible amino acids that determine functional
 RT differences in its isoforms."
 RL Mitochondrion 1:371-379(2002).
 DR EMBL; AB065433; BAB84673.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_car; 3.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 3295 MW; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;
 Best Local Similarity 92.2%; Pred. No. 3e-123;
 Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPADPLAGIAAIAISKTAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
 DB 1 MTEQATSPADPLAGIAAIAISKTAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLAADVGSGEREFRLGDCLVKITSKGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTLAADVGSGEREFRLGDCLVKITSKGIRGLYQGFVS 180
 QY 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPFDTVRBRMM 240
 DB 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPFDTVRBRMM 240
 QY 241 QSGRKGADIMYGTGTCWKRIIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKX 296
 DB 241 QSGRKGADIMYGTGTCWKRIIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKX 296

RESULT 3

Q8JHT0 PRELIMINARY; PRT; 298 AA.
 ID Q8JHT0
 AC Q8JHT0;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Solute carrier family 25 member 5 protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22035902; PubMed=12006978;
 RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
 RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
 RA Hopkins N.;
 RT "Insertional mutagenesis in zebrafish rapidly identifies genes
 RT essential for early vertebrate development."
 RL Nat. Genet. 31:135-140(2002).
 DR EMBL; AF506216; AAM3460.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_car; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;

Query Match 93.7%; Score 1446; DB 13; Length 298;
 Best Local Similarity 91.9%; Pred. No. 8.5e-123;
 Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSPADPLAGIAAIAISKTAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
 DB 1 MTEQATSPADPLAGIAAIAISKTAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLAADVGSGEREFRLGDCLVKITSKGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTLAADVGSGEREFRLGDCLVKITSKGIRGLYQGFVS 180
 QY 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPFDTVRBRMM 240
 DB 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPFDTVRBRMM 240
 QY 241 QSGRKGADIMYGTGTCWKRIIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKXYI 298
 DB 241 QSGRKGADIMYGTGTCWKRIIFRDEGKAFPKGAMSVNLKMGGAFLVLYDELKXYI 298

RESULT 4

O46373 PRELIMINARY; PRT; 298 AA.
 ID O46373
 AC O46373;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Yamaguchi N., Kasai M.;
 RT "Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle."
 RL J. Biochem. 335:541-547(1998).
 CC - - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB009386; BAA23777.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_car; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE, PS00215; MITOCH_CARRIER, 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;
Best Local Similarity 88.9%; Pred. No. 1.3e-120;
Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYKGIIVDCTVR 60
DB 1 MSDQALSLKDFLAGGVAIAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVHQTQFWRYFAGNLSG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVHQTQFWRYFAGNLSG 120
QY 121 GAAGATSLCFYVPLDFAFTRTLAADVGKSTGEREFGDCLVKTSGIRGLYGFSSVS 180
DB 121 GAAGATSLCFYVPLDFAFTRTLAADVGKAAQREFSGDCLVKTSGIRGLYGFSSVS 180
QY 181 VGGIIITRAAFYGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240
DB 181 VGGIIITRAAFYGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240
QY 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGKAFPKGAMSNVLRMGAFVLVLYDELKCVI 298
DB 241 QSGRKGADIMYTGTVDCWKRKIAKDEGAKAFPKGAMSNVLRMGAFVLVLYDELKCVI 298

RESULT 5

QY 0919M9 PRELIMINARY; PRT; 298 AA.
AC 0919M9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrowshahian F., Varmura S.L., Liverage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
Dynamic Patterns of Expression During Development.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL: AF231347; AAF63471.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carrier_3.
DR PRINTS; PRO0926; MITOCARRIER.
DR PROSITE; PRO0784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER, 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;
Best Local Similarity 90.3%; Pred. No. 1.6e-120;
Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYKGIIVDCTVR 60
DB 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOITADKHKGIIDCVRR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVHQTQFWRYFAGNLSG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVHQTQFWRYFAGNLSG 120

QY 121 GAAGATSLCFYVPLDFAFTRTLAADVGKSTGEREFGDCLVKTSGIRGLYGFSSVS 180
DB 121 GAAGATSLCFYVPLDFAFTRTLAADVGKAMREFSGDCLVKTSGIRGLYGFSSVS 180
QY 181 VGGIIITRAAFYGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240
DB 181 VGGIIITRAAFYGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240
QY 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGKAFPKGAMSNVLRMGAFVLVLYDELKCVI 298
DB 241 QSGRKGADIMYTGTVDCWKRKIAKDEGKAFPKGAMSNVLRMGAFVLVLYDELKCVI 298

RESULT 6

QY 09BVI9 PRELIMINARY; PRT; 298 AA.
AC 09BVI9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK078077; BAC37117.1;
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 91.6%; Score 1414; DB 11; Length 298;
Best Local Similarity 88.6%; Pred. No. 6.8e-120;
Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYKGIIVDCTVR 60
DB 1 MGRKALSLKDFLAGGIAAIAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVHQTQFWRYFAGNLSG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVHQTQFWRYFAGNLSG 120
QY 121 GAAGATSLCFYVPLDFAFTRTLAADVGKSTGEREFGDCLVKTSGIRGLYGFSSVS 180
DB 121 GAAGATSLCFYVPLDFAFTRTLAADVGKSSQREFNGJDDCLVKTSGIRGLYGFSSVS 180
QY 181 VGGIIITRAAFYGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240
DB 181 VGGIIITRAAFYGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240
QY 241 QSGRKGADIMYTGTVDCWKRKIFRDEGGKAFPKGAMSNVLRMGAFVLVLYDELKCVI 298
DB 241 QSGRKGADIMYTGTVDCWKRKIAKDEGANAFPKGAMSNVLRMGAFVLVLYDELKCVI 298

RESULT 7

QY 09PRH1 PRELIMINARY; PRT; 298 AA.
AC 09PRH1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE AdP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=8410;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008463; BAA36513.1; -;
 DR EMBL; AB008456; BAA36506.1; -;
 DR EMBL; AB008461; BAA36511.1; -;
 DR EMBL; AB008462; BAA36512.1; -;
 DR InterPro; IPR001993; Mitochondrion carrier.
 DR InterPro; IPR002067; Mitochondrion carrier.
 DR InterPro; IPR002030; Mitochondrion carrier.
 DR Pfam; PF00153; mito_carrier; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;
 Query Match 91.3%; Score 1409; DB 13; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.9e-119;
 Matches 26; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEOATSPADFLAGGAAIAISTAVAPIERVLLLOVHASKQIADKQYKGIIVDCIVR 60
 DB 1 MTEOATSPADFLAGGAAIAISTAVAPIERVLLLOVHASKQIADKQYKGIIVDCIVR 60
 QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRPAGNLASG 120
 DB 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCIVKITSDDIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCIVKITSDDIRGLYOGFSVS 180
 QY 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTIVSWMTAQVTAVAGVSYFPTVRRMM 240
 DB 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTIVSWMTAQVTAVAGVSYFPTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298
 DB 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298
 RESULT 8
 Q9PRH2 PRELIMINARY; PRT; 298 AA.
 AC Q9PRH2;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS *Rana rugosa* (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008460; BAA36510.1; -;
 DR EMBL; AB008458; BAA36508.1; -;
 DR EMBL; AB008459; BAA36509.1; -;

DR InterPro; IPR001993; Mitochondrion carrier.
 DR InterPro; IPR002067; Mitochondrion carrier.
 DR InterPro; IPR002030; Mitochondrion carrier.
 DR Pfam; PF00153; mito_carrier; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225B867599A06 CRC64;
 Query Match 91.3%; Score 1406; DB 13; Length 298;
 Best Local Similarity 88.3%; Pred. No. 3.6e-119;
 Matches 26; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEOATSPADFLAGGAAIAISTAVAPIERVLLLOVHASKQIADKQYKGIIVDCIVR 60
 DB 1 MTEOATSPADFLAGGAAIAISTAVAPIERVLLLOVHASKQIADKQYKGIIVDCIVR 60
 QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRPAGNLASG 120
 DB 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCIVKITSDDIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCIVKITSDDIRGLYOGFSVS 180
 QY 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTIVSWMTAQVTAVAGVSYFPTVRRMM 240
 DB 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTIVSWMTAQVTAVAGVSYFPTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298
 DB 241 QSGRKADIMYTGTVDCMKRIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298
 RESULT 9
 Q9YIC4 PRELIMINARY; PRT; 298 AA.
 AC Q9YIC4;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS *Rana rugosa* (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008457; BAA36507.1; -;
 DR InterPro; IPR001993; Mitochondrion carrier.
 DR InterPro; IPR002067; Mitochondrion carrier.
 DR InterPro; IPR002030; Mitochondrion carrier.
 DR Pfam; PF00153; mito_carrier; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33068 MW; 15B270BD37099A00 CRC64;
 Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 8.3e-119;
 Matches 26; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEOATSPADFLAGGAAIAISTAVAPIERVLLLOVHASKQIADKQYKGIIVDCIVR 60

Db 1 MTDAISFADKDFLAGGAAAIKSTAVAPIERVKLLVOVQHASKOITADKOYKIMDCVVR 60
 QY 1PKEQGVSPFRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDGHTQFMWRPAGNLASG 120
 Db 61 IPKEQGFVSPFRGNLANVIRYFPTQALNFAFKDKYKQIFLDVNDKRTQFMWRPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLADVKGSGTEREFGGLDCLVKITKSDGIRGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDFARTRLADVKGSGTEREFGGLDCLVKITKSDGIRGLYQGFVS 180
 QY 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTVSMIAQTVAAGVSPEDTVRRMM 240
 Db 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTVSMIAQTVAAGVSPEDTVRRMM 240
 QY 241 QSGRKADIMYTGVDKWKRIFRDEGKAFKGAAMSNLRGMAFVLVLDLKKVI 298
 Db 241 QSGRKADIMYTGVDKWKRIFRDEGKAFKGAAMSNLRGMAFVLVLDLKKVI 298

RESULT 10

Q95VX4 PRELIMINARY; PRT; 299 AA.
 AC Q95VX4
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP-ATP translocase.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxId=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 rubripes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401758; AAL02100.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carrier; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3B8CB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;
 Best Local Similarity 81.5%; Pred. No. 1.5e-109;
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MTEOAIKSPADKDFLAGGIAAISKTAIVAPIERVKLLVOVQHASKOIADKOYKGIYDCIVR 60
 Db 1 MPIDVNSLKDPIKAGVAAAIKSTAVAPIERVKLLVOVQHASKOIADKOYKGIYDCIVR 60
 QY 61 IPKEQGVSPFRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDGHTQFMWRPAGNLASG 120
 Db 61 IPKEQGVSPFRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDGHTQFMWRPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLADVKGSGTEREFGGLDCLVKITKSDGIRGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDFARTRLADVKGSGTEREFGGLDCLVKITKSDGIRGLYQGFVS 180
 QY 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTVSMIAQTVAAGVSPEDTVRRMM 240
 Db 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTVSMIAQTVAAGVSPEDTVRRMM 240
 QY 241 QSGRKADIMYTGVDKWKRIFRDEGKAFKGAAMSNLRGMAFVLVLDLKKVI 298
 Db 241 QSGRKADIMYTGVDKWKRIFRDEGKAFKGAAMSNLRGMAFVLVLDLKKVI 298

RESULT 11
 Q91336 PRELIMINARY; PRT; 317 AA.
 ID Q91336

AC Q91336;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (wood frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxId=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cai Q., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress";
 RL Biochim. Biophys. Acta 1353:69-78 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Cai Q., Storey K.B.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; U44832; AAA97882.2; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carrier; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
 Best Local Similarity 86.8%; Pred. No. 8.2e-106;
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTEOAIKSPADKDFLAGGIAAISKTAIVAPIERVKLLVOVQHASKOIADKOYKGIYDCIVR 60
 Db 1 MTDAISFADKDFLAGGAAAIKSTAVAPIERVKLLVOVQHASKOITADKOYKIMDCVVR 60
 QY 61 IPKEQGVSPFRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDGHTQFMWRPAGNLASG 120
 Db 61 IPKEQGVSPFRGNLANVIRYFPTQALNFAFKDKYKQIFLDVNDKRTQFMWRPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLADVKGSGTEREFGGLDCLVKITKSDGIRGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDFARTRLADVKGSGTEREFGGLDCLVKITKSDGIRGLYQGFVS 180
 QY 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTVSMIAQTVAAGVSPEDTVRRMM 240
 Db 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTVSMIAQTVAAGVSPEDTVRRMM 240
 QY 241 QSGRKADIMYTGVDKWKRIFRDEGKAFK 272
 Db 241 QSGRKADIMYTGVDKWKRIFRDEGKAFK 272

RESULT 12

Q81RA0 PRELIMINARY; PRT; 312 AA.
 AC Q81RA0
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG16944-PC.
 GN SE8B.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
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Db 129 TSLCFVPLDFAIRTLADTGKG-QREFTLGNCLAKIFKSDGLVGLRGFVSGII 187
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DB 188 IYRAAYFGVYDTAKGMLPDPKNTIIVSWMIQVTAAGVSVFPDTRRRMMQSGRK 247
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DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025798; AAB87883.1; -.
DR FlyBase; FBgn0023292; Dpse\seeb.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR Pfam; PF00153; mito_cartr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT * NON TER
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Query Match 77.0%; Score 1187.5; DB 5; Length 288;
Best Local Similarity 80.7%; Pred. No..2.2e-99;
Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

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QY 125 ATSLCFVYPLDFAIRTLADVGKSGTEREPRGLDCLVKITKSDGIRGLYOGFSVVOGI 184
DB 127 ATSLCFVYPLDFAIRTLADVGKSG-QREFTLGNCLTKIFKSDGLVGLYRGFVSGOI 185
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AC 044094;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

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DE ADP/ATP translocase (Fragment).
GN SESB.
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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
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RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025799; AAB87884.1; -.
DR FlyBase; FBgn0023237; Dpse\seeb.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR Pfam; PF00153; mito_cartr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT * NON TER
FT 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
Best Local Similarity 80.4%; Pred. No. 5e-99;
Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISRKDLAGIAAISKTAVAPIERVKLLQVQHASKQIADQYKGIYDCVIRIPE 64
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 Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:10:04 ; Search time 31 Seconds
(without alignments)
1795.292 Million cell updates/sec

Title: US-09-185-904A-33
Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGIAAA.....LRMGAFVLYDELKKVI 298

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues
Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	US-09-811-094-33	Sequence 33, Appl
2	1543	100.0	298	US-09-810-644-33	Sequence 33, Appl
3	1543	100.0	298	US-09-185-904A-33	Sequence 33, Appl
4	1454	94.2	298	US-09-811-094-33	Sequence 32, Appl
5	1454	94.2	298	US-09-810-644-33	Sequence 32, Appl
6	1454	94.2	298	US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.8	297	US-09-811-094-31	Sequence 31, Appl
8	1385.5	89.8	297	US-09-810-644-31	Sequence 31, Appl
9	1385.5	89.8	297	US-09-185-904A-31	Sequence 31, Appl
10	811	52.6	179	US-10-029-386-32501	Sequence 33501, A
11	788.5	51.1	301	US-10-032-585-7194	Sequence 252, Ap
12	760.5	49.3	318	US-09-801-358-252	Sequence 170, App
13	749.5	48.6	386	US-09-734-569-170	Sequence 338, Ap
14	737	47.8	308	US-10-128-714-3338	Sequence 8338, Ap
15	737	47.8	308	US-10-128-714-8338	Sequence 8338, Ap

16	734.5	47.6	381	12	US-10-141-478A-2	Sequence 2, Appli
17	686	44.5	677	12	US-10-259-165-192	Sequence 192, App
18	518	33.6	132	9	US-09-925-301-1459	Sequence 1459, Ap
19	423	27.4	87	9	US-09-864-761-36440	Sequence 36440, A
20	368	23.8	475	10	US-09-777-921A-4	Sequence 4, Appli
21	368	23.8	477	10	US-09-777-921A-2	Sequence 2, Appli
22	333.5	21.6	410	10	US-09-777-921A-5	Sequence 5, Appli
23	326	21.1	384	12	US-10-094-749-1789	Sequence 1789, Ap
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25	314	20.3	469	9	US-09-989-723-289	Sequence 289, App
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29	314	20.3	469	10	US-09-989-732-289	Sequence 289, App
30	314	20.3	469	10	US-09-989-733-289	Sequence 289, App
31	314	20.3	469	10	US-09-989-734-289	Sequence 289, App
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34	314	20.3	469	10	US-09-989-737-289	Sequence 289, App
35	314	20.3	469	10	US-09-989-738-289	Sequence 289, App
36	314	20.3	469	10	US-09-989-739-289	Sequence 289, App
37	314	20.3	469	10	US-09-989-740-289	Sequence 289, App
38	314	20.3	469	10	US-09-989-741-289	Sequence 289, App
39	314	20.3	469	10	US-09-989-742-289	Sequence 289, App
40	314	20.3	469	10	US-09-989-743-289	Sequence 289, App
41	314	20.3	469	10	US-09-989-744-289	Sequence 289, App
42	314	20.3	469	10	US-09-989-745-289	Sequence 289, App
43	314	20.3	469	10	US-09-989-746-289	Sequence 289, App
44	314	20.3	469	10	US-09-989-747-289	Sequence 289, App
45	314	20.3	469	11	US-09-989-748-289	Sequence 289, App

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US20010044149A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleverger, William
APPLICANT: Wile, Sandra Eileen
APPLICANT: Wile, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33
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Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MTEQAISFAKDFLAGIAAAISKTAFAPIREVKLLLOVHASKOIADKQYIVDCIVR 60
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RESULT 2

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US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yachong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-33

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Query Match 100.0%; Score 1543; DB 9; Length 298;
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 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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US-09-185-904A-33
; Sequence 33, Application US/09185904A
; Patent No. US2002017185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

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; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-33

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Db      61  IPKEQGLSFWRGMLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
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Db      181  VGGIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTAVAGVVSYPEDTVRRMM 240
QY      241  QSGRKGADIMYTGTVDCWKRIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298
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RESULT 4

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; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

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 Best Local Similarity 92.6%; Pred. No. 3.5e-147;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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 Qy 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELKX 296
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RESULT 5
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 ; Sequence 32, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Moos, Walter H.
 APPLICANT: Pei, Yanzhong
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 FILE REFERENCE: 660088.420D3
 CURRENT APPLICATION NUMBER: US/09/810.644
 CURRENT FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 32
 LENGTH: 298
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-810-644-32

Query Match 94.2%; Score 1454; DB 9; Length 298;
 Best Local Similarity 92.6%; Pred. No. 3.5e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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 Db 61 IPKEQVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
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 Db 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTSGINGLYOGFVNS 180
 Qy 181 VOGIIYRAAYFGYVDTAKGMLPDKNTHIVSWMIQOTYAVAGVSYPPDYRRRRMM 240
 Db 181 VOGIIYRAAYFGYVDTAKGMLPDKNTHIVSWMIQOTYAVAGVSYPPDYRRRRMM 240
 Qy 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELKX 296
 Db 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDEIKX 296

RESULT 6
 US-09-185-904A-32
 ; Sequence 32, Application US/09185904A
 ; Patent No. US20020177185A1
 ; GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 THEREFOR
 FILE REFERENCE: 660088.420
 CURRENT APPLICATION NUMBER: US/09/185.904A
 CURRENT FILING DATE: 1998-11-03
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 32
 LENGTH: 298
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-185-904A-32

Query Match 94.2%; Score 1454; DB 10; Length 298;
 Best Local Similarity 92.6%; Pred. No. 3.5e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTEOATSPKADFLAGGIAAISTKAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60
 Db 1 MTDALSTAKDFLAGGVAIAISTKAVAPIERVKLLLOVQHASKOITADKQYKGIIDCVR 60
 Qy 61 IPKEQVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 Db 61 IPKEQVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 Qy 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTSGINGLYOGFVNS 180
 Db 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTSGINGLYOGFVNS 180
 Qy 181 VOGIIYRAAYFGYVDTAKGMLPDKNTHIVSWMIQOTYAVAGVSYPPDYRRRRMM 240
 Db 181 VOGIIYRAAYFGYVDTAKGMLPDKNTHIVSWMIQOTYAVAGVSYPPDYRRRRMM 240
 Qy 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELKX 296
 Db 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDEIKX 296

RESULT 7
 US-09-811-094-31
 ; Sequence 31, Application US/09811094
 ; Patent No. US20010044144A1
 ; GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Moos, Walter H.
 APPLICANT: Pei, Yanzhong
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 FILE REFERENCE: 660088.420D4
 CURRENT APPLICATION NUMBER: US/09/811.094
 CURRENT FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 37

SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-811-094-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAIISFADPLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKOYKGIIVDCIVR 60
 DB 1 MGDHAWSFLLKDFLAGAIAAAVSKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVRR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRHQPWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRHQPWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLAADVGSRTREFRGLGDCIVKITSKDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREHFGDLCIIRKFSKDGIRGLYOGFSVS 179
 QY 181 VQGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDVRRRMM 240
 DB 180 VQGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDVRRRMM 239
 QY 241 QSGRKADIMYTGTVDCWKRKIFRDEGKAFKGAWSNVLRMGAFVLVYDELKXYI 298
 DB 240 QSGRKADIMYTGTVDCWKRKIADEGAKAFKGAWSNVLRMGAFVLVYDELKXYI 297

RESULT 8

US-09-810-644-31
 ; Sequence 31, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Cleverger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pei, Yanzhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810.644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-810-644-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAIISFADPLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKOYKGIIVDCIVR 60
 DB 1 MGDHAWSFLLKDFLAGAIAAAVSKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVRR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRHQPWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRHQPWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLAADVGSRTREFRGLGDCIVKITSKDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREHFGDLCIIRKFSKDGIRGLYOGFSVS 179

DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREHFGDLCIIRKFSKDGIRGLYOGFSVS 179
 QY 181 VQGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDVRRRMM 240
 DB 180 VQGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDVRRRMM 239
 QY 241 QSGRKADIMYTGTVDCWKRKIFRDEGKAFKGAWSNVLRMGAFVLVYDELKXYI 298
 DB 240 QSGRKADIMYTGTVDCWKRKIADEGAKAFKGAWSNVLRMGAFVLVYDELKXYI 297

RESULT 9

US-09-185-904A-31
 ; Sequence 31, Application US/09185904A
 ; Patent No. US20020177185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Cleverger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185.904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-185-904A-31

Query Match 89.8%; Score 1385.5; DB 10; Length 297;
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAIISFADPLAGGIAAIAISKTAVAPIERVKLLLOVQHASKOIAADKOYKGIIVDCIVR 60
 DB 1 MGDHAWSFLLKDFLAGAIAAAVSKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVRR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRHQPWRYPAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRHQPWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLAADVGSRTREFRGLGDCIVKITSKDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREHFGDLCIIRKFSKDGIRGLYOGFSVS 179
 QY 181 VQGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDVRRRMM 240
 DB 180 VQGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDVRRRMM 239
 QY 241 QSGRKADIMYTGTVDCWKRKIFRDEGKAFKGAWSNVLRMGAFVLVYDELKXYI 298
 DB 240 QSGRKADIMYTGTVDCWKRKIADEGAKAFKGAWSNVLRMGAFVLVYDELKXYI 297

RESULT 10

US-10-029-386-32501
 ; Sequence 32501, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
 ; FILE REFERENCE: AEOMICA-X-2


```

; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinhold, Andreas
; APPLICANT: Citpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Duwenig, Elke
; APPLICANT: Freund, Annette
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reeki, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734.569
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-170

```

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Query Match          48.6%; Score 749.5; DB 9; Length 386;
Best Local Similarity 53.4%; Pred. No. 1.3e-71;
Matches 157; Conservative 44; Mismatches 84; Indels 9; Gaps 5;

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QY 7 SPKADPLAGIAAIAIKTANAPIERVKLLIQVQ-HASKQIAADKQYGVDCIVIRPEQ 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 SFWDFMGVSAVSAVSTAAPIERVKLLIQVQEMKSGRLSHYKGISCFERTYKDE 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 66 GVSFWRGNTLVNVRYPPTQALNFAFKDKYQIFLGVDKHTQWRFPAGNLASGGA 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 GMSVLSMRGNTLVNVRYPPTQALNFAFKDYKSLFGYKDK-DGYKWPAGNLASGGA 202
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 126 TSLCFVYPLDPAFRLAADV--GKSGTEREFRGLDCLVTKTSDGIRGLYQGSVS 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 SLSLFVYSLDYARTRLANDAKSKSGGERQFNGLVYVKTLATDGIAGYRFAISCA 262
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 GIITIRAAVFGVYDTAKG-MLPDPKNTHTIVSWMIAQVTAVAGVSVFDTVRRMMQ 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 263 GIIVYRGVFGVYDLPVVLVGLNLEGNFLASFLGAGITGAGLASYPIDTVRRMMT 322
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 242 SGRKADIMVTGVDCWKRIFRDEGKAFKFGKMSNVLRGMGAFVLVYDELK 295
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 323 SGEA--VKYNGSMDAPKQILAKEGAKSLFKGAGANTILRAVAGVLSYDQVLQ 373
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 14
US-10-128-714-3338
; Sequence 3338, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskinin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899

```

```

; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3338
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3338

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```

Query Match          47.8%; Score 737; DB 15; Length 308;
Best Local Similarity 51.7%; Pred. No. 2.1e-70;
Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;

```

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QY 7 SPKADPLAGIAAIAIKTANAPIERVKLLIQVQ-HASKQIAADKQYGVDCIVIRPEQ 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 AFTDSFVGVSAVSAVSTAAPIERVKLLIQVQEMKSGRLSHYKGISCFERTYKDE 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 EGVLSFWRGNTLVNVRYPPTQALNFAFKDKYQIFLGVDKHTQWRFPAGNLASGGA 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 AEGVLSMRGNTLVNVRYPPTQALNFAFRDYSMFAKKDR-DGYAKMMGNLASGGA 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 GATSLCFVYPLDPAFRLAADV--GKSGTEREFRGLDCLVTKTSDGIRGLYQGSVS 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 GATSLFVYSLDYARTRLANDAKSKSGGERQFNGLIDVRKTLASDGIAGYRGSPSV 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 QGIIIRAAVFGVYDTAKG-MLPDPKNTHTIVSWMIAQVTAVAGVSVFDTVRRMM 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 LGIVYRGVFGVYDLPVVLVGLNLEGNFLASFLGAGITGAGLASYPIDTVRRMM 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 QSRKADIMVTGVDCWKRIFRDEGKAFKFGKMSNVLRGMGAFVLVYDELK 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 TSGEA--VKYKSLDPAKQILAKEGAKSLFKGAGANTILRAVAGVLSYDQVL 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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```

RESULT 15
US-10-128-714-8338
; Sequence 8338, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskinin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8338
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8338

```

```

Query Match          47.8%; Score 737; DB 15; Length 308;
Best Local Similarity 51.7%; Pred. No. 2.1e-70;
Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;

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Db 241 QSGRKADIMYTGVCWRKIFRDEGGKAFKGAWSNVLKRGMGAFVLVLYDELKVI 298

```

RESULT 2
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Velicelbel, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48

Query Match          94.2%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 5.2e-15;
Matches 274; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
DB 1 MTDALSFADFLAGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
QY 61 IPKEQGLSFWRNLANVIRYPTQALNFAFKDXYKQIFLGVDKHTQFMRYPAGNLASG 120
DB 61 IPKEQGLSFWRNLANVIRYPTQALNFAFKDXYKQIFLGVDKHTQFMRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADAVGKSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
DB 121 GAAGATSLCFVYPLDFARTLADAVGKSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
QY 181 VQGIIRYRAAFVGYVTAKGMLPDPKNTIIVSWMIQOTYAVAGVSYFPDTRRRMM 240
DB 181 VQGIIRYRAAFVGYVTAKGMLPDPKNTIIVSWMIQOTYAVAGVSYFPDTRRRMM 240
QY 241 QSGRKADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAFVLYYDEIKK 296
DB 241 QSGRKADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAFVLYYDEIKK 296

RESULT 3
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-Oct-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10

Query Match          91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.9e-151;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
DB 1 MGDQALSFKDPLAGIAAIAVSKTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
QY 61 IPKEQGLSFWRNLANVIRYPTQALNFAFKDXYKQIFLGVDKHTQFMRYPAGNLASG 120
DB 61 IPKEQGLSFWRNLANVIRYPTQALNFAFKDXYKQIFLGVDKHTQFMRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADAVGKSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
DB 121 GAAGATSLCFVYPLDFARTLADAVGKSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
QY 181 VQGIIRYRAAFVGYVTAKGMLPDPKNTIIVSWMIQOTYAVAGVSYFPDTRRRMM 240
DB 181 VQGIIRYRAAFVGYVTAKGMLPDPKNTIIVSWMIQOTYAVAGVSYFPDTRRRMM 240
QY 241 QSGRKADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAFVLYYDEIKK 298
DB 241 QSGRKADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAFVLYYDEIKK 298

RESULT 4
US-09-434-354-47
; Sequence 47, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Velicelbel, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien

```


US-09-434-354-47

Query Match 89.8%; Score 1385.5; DB 4; Length 297;
 Best Local Similarity 87.2%; Pred No. 2,9e-148;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MTEQASPKDFLAGIAAISKTAIVAPIERVKLLQVQHASKQIAADKQYKGIIVDCIVR 60
 Db 1 MGDHMSFLKDFLAGVAVAASKTAVAPIERVKLLQVQHASKQISAKQYKGIIDCVR 60
 Qy 61 IPKEGVLSFWRGNLANIRIRPTQALNPAFKQXKQKQIFLGVDVGHQTFWRFEAGNLASG 120
 Db 61 IPKEGVLSFWRGNLANIRIRPTQALNPAFKQXKQKQIFLGVDVGHQTFWRFEAGNLASG 120
 Qy 121 GAAGATSLCFYVPLDFARTLADADVGKSGTEREFGLDGCYKIRKSGDGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDFARTLADADVGRR-AQREFFGLDGCITIKRSGDGLYQGFVS 179
 Qy 181 VGGIIYRAAYFGVYDTAKGMLPDKNTHIVVSMIAQTVAAGVSVYFDTVRRMM 240
 Db 180 VGGIIYRAAYFGVYDTAKGMLPDKNVHIFVSMIAQSVTAVAGLLSYFDTVRRMM 239
 Qy 241 QSGRGALIMTGTDCRRKIFRDEGGAFFFGKANSNLRGMGAFVLYLDELKVI 238
 Db 240 QSGRGADIMTGTVDCCRKIAKDEGAKAFFGKANSNLRGMGAFVLYLDELKVI 237

RESULT 5
 US-09-996-243-289

/ Sequence 289, Application US/09996243

/ Patent No. 6478825

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi J.

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Boctstein, David

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Eaton, Dan L.

/ APPLICANT: Ferrara, Napoleone

/ APPLICANT: Fong, Sherman

/ APPLICANT: Gerber, Hanspeter

/ APPLICANT: Gerritsen, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Kljavin, Ivar J.

/ APPLICANT: Napier, Mary A.

/ APPLICANT: Pan, James

/ APPLICANT: Paoni, Nicholas F.

/ APPLICANT: Roy, Margaret Ann

/ APPLICANT: Stewart, Timothy A.

/ APPLICANT: Tunas, Daniel

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Williams, P. Mickey

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ TITLE OF INVENTION: Acids Encoding the Same

/ FILE REFERENCE: P2730PCL3

/ CURRENT APPLICATION NUMBER: US/09/996,243

/ PRIOR FILING DATE: 2001-11-14

/ PRIOR APPLICATION NUMBER: 60/049787

/ PRIOR FILING DATE: 1997-06-16

/ PRIOR APPLICATION NUMBER: 60/062250

/ PRIOR FILING DATE: 1997-10-17

/ PRIOR APPLICATION NUMBER: 60/065186

/ PRIOR FILING DATE: 1997-11-12

/ PRIOR APPLICATION NUMBER: 60/065311

/ PRIOR FILING DATE: 1997-11-13

/ PRIOR APPLICATION NUMBER: 60/066770

/ PRIOR FILING DATE: 1997-11-24

/ PRIOR APPLICATION NUMBER: 60/075945

/ PRIOR FILING DATE: 1998-02-25

/ PRIOR APPLICATION NUMBER: 60/089598

/ PRIOR APPLICATION NUMBER: 60/078910
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/083322
 / PRIOR FILING DATE: 1998-04-28
 / PRIOR APPLICATION NUMBER: 60/084600
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/087106
 / PRIOR FILING DATE: 1998-05-28
 / PRIOR APPLICATION NUMBER: 60/087607
 / PRIOR FILING DATE: 1998-06-02
 / PRIOR APPLICATION NUMBER: 60/087609
 / PRIOR FILING DATE: 1998-06-02
 / PRIOR APPLICATION NUMBER: 60/087759
 / PRIOR FILING DATE: 1998-06-02
 / PRIOR APPLICATION NUMBER: 60/087827
 / PRIOR FILING DATE: 1998-06-03
 / PRIOR APPLICATION NUMBER: 60/088021
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088025
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088026
 / PRIOR FILING DATE: 1998-06-04
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 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088029
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 / PRIOR APPLICATION NUMBER: 60/088030
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088033
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088326
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088167
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088202
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088212
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088217
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088655
 / PRIOR FILING DATE: 1998-06-09
 / PRIOR APPLICATION NUMBER: 60/088734
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088738
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088742
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088810
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088824
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088826
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088858
 / PRIOR FILING DATE: 1998-06-11
 / PRIOR APPLICATION NUMBER: 60/088861
 / PRIOR FILING DATE: 1998-06-11
 / PRIOR APPLICATION NUMBER: 60/088876
 / PRIOR FILING DATE: 1998-06-11
 / PRIOR APPLICATION NUMBER: 60/089105
 / PRIOR FILING DATE: 1998-06-12
 / PRIOR APPLICATION NUMBER: 60/089440
 / PRIOR FILING DATE: 1998-06-16
 / PRIOR APPLICATION NUMBER: 60/089512
 / PRIOR FILING DATE: 1998-06-16
 / PRIOR APPLICATION NUMBER: 60/089514
 / PRIOR FILING DATE: 1998-06-16
 / PRIOR APPLICATION NUMBER: 60/089532
 / PRIOR FILING DATE: 1998-06-17
 / PRIOR APPLICATION NUMBER: 60/089538
 / PRIOR FILING DATE: 1998-06-17
 / PRIOR APPLICATION NUMBER: 60/089598

PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089600
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089801
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089907
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089908
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/089947
 PRIOR FILING DATE: 1998-06-19
 PRIOR APPLICATION NUMBER: 60/089948
 PRIOR FILING DATE: 1998-06-19
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 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090252
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090254
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090349
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090355
 PRIOR FILING DATE: 1998-06-23
 PRIOR APPLICATION NUMBER: 60/090429
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090431
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090435
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090444
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090445
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090472
 PRIOR FILING DATE: 1998-06-24
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 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090542
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090557
 PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090676
 PRIOR FILING DATE: 1998-06-25
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 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090690
 PRIOR FILING DATE: 1998-06-25
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 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/090863
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: 60/091360
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091478
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091544
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 20.3%; Score 314; DB 4; Length 469;
 Best Local Similarity 30.1%; Pred. No. 7.8e-27;
 Matches 89; Conservative 60; Mismatches 115; Indels 32; Gaps 11;

QY 10 KDFLAGGIAAISKTVAPRIERYKLLVOHAKQJLAADQYGYVDCIRIKEGVLS 69
 DB 188 RHLVAGGAGAVSRTCTAPDRUKVLMOV-HASR-----SNNMCIVGGFTQMTREGGARS 241
 QY 70 FMRGNLANVIRYPTOLNFAFDKRYKQIFLGVDKHTQFWRYPAGNLASGAAGATSLC 129
 DB 242 LMRGNGINVLKIPESAIKFMAYEQIKR--LVGSDQET--LRIHERLVAGSLAGATAOS 296
 QY 130 FVYPLDFARTRLADYVKGSGTEREFRLGDCLVKITKSDGIRGLYOGFSVSVOGIITRYA 189
 DB 297 SIYPMEVILKTRMA--LRKTS---QYSGMLDCARRILAREGVAAFYKGYVNMMLGIIPYAG 351
 QY 190 AYFGVYDTAKG-----LPDPKNTHIYVSMIMIQTVAAVAG--VVSYPFDTVRRMM 240
 DB 352 IDLAIVETLLNAMLQHYAVNSADPG---VFVLLACGTMSSTGQLASTYPLALVTRTMOA 407
 QY 241 QSGRKADIMYGTQVDCKRIFPDEGGKAFKGAWSVLRGMGAGAV-LVLYDELK 295
 DB 408 QASIEGAPETWSSL--FKHILTEGAFGLYRLGLANPMKVIYAVSISYVYENLK 461

RESULT 6
 US-09-188-930-339
 ; Sequence 339, Application US/09188930A
 ; Patent No. 6150502
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Iorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James Greg
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; FILE REFERENCE: 11000.1011c1
 ; CURRENT APPLICATION NUMBER: US/09/188,930A
 ; CURRENT FILING DATE: 1998-11-09
 ; NUMBER OF SEQ. ID NOS: 348
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 339
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-188-930-339

Query Match 20.2%; Score 311; DB 3; Length 469;
 Best Local Similarity 29.4%; Pred. No. 1.7e-26;
 Matches 88; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

QY 10 KDFLAGGIAAISKTVAPRIERYKLLVOHAKQJLAADQYGYVDCIRIKEGVLS 69
 DB 188 RHLVAGGAGAVSRTCTAPDRUKVLMOV-HASR-----SNNMCIVGGFTQMTREGGARS 241
 QY 70 FMRGNLANVIRYPTOLNFAFDKRYKQIFLGVDKHTQFWRYPAGNLASGAAGATSLC 129
 DB 242 LMRGNGINVLKIPESAIKFMAYEQIKR--LVGSDQET--LRIHERLVAGSLAGATAOS 296
 QY 130 FVYPLDFARTRLADYVKGSGTEREFRLGDCLVKITKSDGIRGLYOGFSVSVOGIITRYA 189

Db 297 SIYMEVLTAKMMA--LRKTG---QYSGMLDCARILAEKGAFAFYKGIYPMNLGIIPYAG 351
 QY 190 AYFGYDTAKGMLPDPKATHI-----VVSMTIAQVTAAG--VVSYPPTVRR 237
 Db 352 IDLAVERL-----KNTWLORYAVNSADPGVFLILACGIISSYCGQIASIPILAVRTR 404
 QY 238 MMOSGRKADIMYTGTVDCWRKIFRDEGKAFKFGANSVNLKMGGAFAV-LVLYDELK 295
 Db 405 MOAQASIGAPVETMSSL--FKQILRTGAGFGLYHGLAPNFMKVI PAVISISVYVENLK 461

RESULT 7
 US-09-312-283C-339
 ; Sequence 339, Application US/09312283C
 ; Patent No. 6573095
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011C2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 339
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-312-283C-339

Query Match 20.2%; Score 311; DB 4; Length 469;
 Best Local Similarity 29.4%; Pred. No. 1.7e-26;
 Matches 88; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

QY 10 KDFLAGGIAAIAISTKAVAPIERVKLLIYOVHASKIADADKQYKIVDCIVIRPEQVLS 69
 Db 188 RHLVAGGAGAVSRCTPLRLKVLMOV-HASR-----SNMCIYGGFTQMIREGAKS 241
 QY 70 FMRGLAVIVIRYFPFOALNFAFKDKYKQIFLGVDVKTQFWRYPAGNLSGGAAGATSLC 129
 Db 242 LMRGNIVLKIAPSAIKFPAEOMK--LVGSDQET--LRHERLVASGLAGALIQS 296
 QY 130 FVYPLDFARTRLADVGSATEREFGDCLVITKSDGIRGLYOGFSVSVOGIIVYRA 189
 Db 297 SIYMEVLTAKMMA--LRKTG---QYSGMLDCARILAEKGAFAFYKGIYPMNLGIIPYAG 351
 QY 190 AYFGYDTAKGMLPDPKATHI-----VVSMTIAQVTAAG--VVSYPPTVRR 237
 Db 352 IDLAVERL-----KNTWLORYAVNSADPGVFLILACGIISSYCGQIASIPILAVRTR 404
 QY 238 MMOSGRKADIMYTGTVDCWRKIFRDEGKAFKFGANSVNLKMGGAFAV-LVLYDELK 295
 Db 405 MOAQASIGAPVETMSSL--FKQILRTGAGFGLYHGLAPNFMKVI PAVISISVYVENLK 461

RESULT 8
 US-09-482-273-118
 ; Sequence 118, Application US/09482273
 ; Patent No. 6534631
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: P2030P1
 ; CURRENT APPLICATION NUMBER: US/09/482,273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921

EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/092,922
 EARLIER FILING DATE: 1998-07-15
 EARLIER APPLICATION NUMBER: 60/092,956
 EARLIER FILING DATE: 1998-07-15
 NUMBER OF SEQ ID NOS: 267
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 118
 LENGTH: 335
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (335)
 OTHER INFORMATION: Xaa equals stop translation
 US-09-482-273-118

Query Match 18.5%; Score 286; DB 4; Length 335;
 Best Local Similarity 29.0%; Pred. No. 6.9e-24;
 Matches 87; Conservative 50; Mismatches 133; Indels 30; Gaps 8;

QY 10 KDFLAGGIAAIAISTKAVAPIERVKLLIYOVHASKIADADKQYKIVDCIVIRPEK 64
 Db 51 KPFYGGGLASIVAEFGTFPVDLTTRLOQVQGSIDARFKEI---KYRGMFHALFRICKE 106
 QY 65 QGVLSFMRGLAVIVIRYFPFOALNFAFKDKYKQIFLGVDVKTQFWRYPAGNLSGGAAG 124
 Db 107 EGVLAISGIAIPALLRQASGTITKIGIYOSLKRLEVERLEDET---LILNMCGVSVG 161
 QY 125 ATSLCFYPLDFARTRLADVGSATEREFGDCLVITKSDGIRGLYOGFSVSVOGI 184
 Db 162 VISSTIANPDTVLKIRMQA---QGSIFQSGMIGS-FIDLYQDEGTFGLMRGVVPTAORA 216
 QY 185 ILYAAIFGYVDK-----GMLPDPKATHIYVSMIAQVTAAGVVSYPPTVRRM 238
 Db 217 AIVGVELPYVDITKQHLISGMWGDITLHFVSSF---TCGLAGALASNPVDVVRTRM 272
 QY 239 MMOSGRKADIMYTGTVDCWRKIFRDEGKAFKFGANSVNLKMGGAFAV-LVLYDELK 297
 Db 273 MNOQAIYGVVDLYKGTVDGILKMKKEGFPALYKGFPMNLRISPNWIIFFITYEQLRRL 332

RESULT 9
 US-09-501-558-2
 ; Sequence 2, Application US/09501558
 ; Patent No. 6403784
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Mathur, Brian
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sande, Arthur T.
 ; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
 ; FILE REFERENCE: LEX-0012-USA
 ; CURRENT APPLICATION NUMBER: US/09/501,558
 ; CURRENT FILING DATE: 2000-02-09
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 291
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-501-558-2

Query Match 18.4%; Score 283.5; DB 4; Length 291;
 Best Local Similarity 28.9%; Pred. No. 1.1e-23;
 Matches 87; Conservative 54; Mismatches 129; Indels 31; Gaps 9;

QY 10 KDFLAGGIAAIAISTKAVAPIERVKLLIYOVHASKIADADKQYKIVDCIVIRPEK 64
 Db 7 KPFYGGGLASITACGTFPIDLTTRLOQVQGSIDARFKEI---RYRGMHLALVRIGRE 62
 QY 65 QGVLSFMRGLAVIVIRYFPFOALNFAFKDKYKQIFLGVDVKTQFWRYPAGNLSGGAAG 124

Db 63 EGKALYSGLAPMMLQASVGTIKICTYOSLKRLLPIERPEBDT-----LPINIVICGLISG 117
 Oy 125 ATSLCFYPLPDPARTRLADVKGSGTREFRGLGDLCKITKSDGIRGLYOGFESVVOGI 184
 Db 118 VIISTIANPFDVLIKIRMOA---OSNTIQ--GAMIGAPNNITYOQESTRGLMGSVELTAORA 172
 Oy 185 IIVRAAYFGVYDPAK-----GMLPDPKNTHTIVSMMTAQITVAVAGVSYSPEDTVRRM 238
 Db 173 AIIVGVELPYVYDITKTHLLISGLMGVTVTHFLSSF-----TCGLAGALASNPVVVVRTRM 228
 Oy 239 MMOSG-RKGAIDIYGTGVDCWRKIFPDEBCKRFPFGAGANSVLR-CMGCAFLVLYDELKX 286
 Db 229 MNGRVLRDGCSCSYTGTITDCLQGTWNBESFPFLYVYGGFPMNLRLQPMNIIFFVYIYEDLKK 288
 Oy 297 V 297
 Db 289 L 289

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RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: CH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24*
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-160-119-4

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[illegible]

RESULT 11.
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219

```

: GENERAL INFORMATION:
: APPLICANT: KRIEF, STEPHANE
: APPLICANT: SOUCHET, MICHEL
: APPLICANT: BRIL, ANTOINE
: TITLE OF INVENTION: NOVEL
: FILE REFERENCE: GH-30985
: CURRENT APPLICATION NUMBER: US/09/160,119A
: CURRENT FILING DATE: 1998-09-24
: EARLIER APPLICATION NUMBER: EP 97402511.6
: EARLIER FILING DATE: 1997-10-23
: EARLIER APPLICATION NUMBER: EP 98401655.0
: EARLIER FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 674
: TYPE: PR1
: ORGANISM: HOMO SAPIENS
US-09-160-119-2

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[illegible]

```

RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-142-565-2

Query Match      17.2%;   Score 265;   DB 3;   Length 312
Best Local Similarity 27.1%;   Pred. No. 1,5e-21;

```

Matches 82; Conservative 52; Mismatches 145; Indels 24; Gaps 8;

QY 7 SFAPKFLAGGIAAISTKAVAPIERVKLLQVOV--HASKQIADKQYKGIIVCIVRIPE 64
 12 TMAVVFLEAGTACRADLVTFPLDTRAKVRLQIGESQAVQTRALVQYRGVLTITMWT 71
 Db 65 QCVLSFWKGNLANVIRYFTQALNFAKDKYKQIFL-GGVDKHTQFWRYPAGNLASGGA 123
 72 EGPSPYNGLVAGLQROMSPASIRIGLYDSVKQVTPKADNSLITRILA-----GCTT 126
 QY 124 CATSLCFYVPLDPATRLAADV--GKSGTEREFRGLGCLVKITSDGIRGLYOGFSVS 181
 127 GAMVATCAQPTVVKVRFOQASIHLPGRSDRKSGMTAYRTIAREBGRGLMKGTLPVI 186
 Db 182 QGIIIRAYAFGVYDTAKGMLPDPKXTHIVSWMIAQTVA-----VAGVSYPPDTYR 236
 187 MRNALVNCAEVTVTILKEKLD---YHLLTNFPCHFYASAGAGFCATVVASPVAVKT 243
 QY 237 RMMQSGRKADIMYGTVDCKRKIFRDEGKAFKGAWSNVL-R-GMGAFVLVLYDELK 295
 244 RYM-----NSPPQYFSPFLDCMKVAVQEGPTAFYKGFSPFLRGLGSMNVVVFVTEQLK 298
 QY 236 KVI 298
 Db 299 RAL 301

RESULT 13
 US-08-518-878B-56
 ; Sequence 56, Application US/08518878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; * COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/518,878B
 ; FILING DATE: 23-AUG-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-036
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;
 Best Local Similarity 24.9%; Pred. No. 6e-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISTKAVAPIERVKLLQVOHASK--QIADKQYKGIIVCIVRIPEQGV 68

Db 7 FLAGGTAACIADLTFPDLTAKVRLQIGESQGPVATVSAQYRGVMTITLMTWTEGPR 66
 QY 69 SFMRGNLANVIRYFTQALNFAKDKYKQIFLGVVDKHTQFWRYPAGNLASGAAGATSL 128
 Db 67 SLVNGLVAGLQROMSPASIRIGLYDSVKQVTPKADNSLITRILA-----GCTT 126
 QY 129 CFVYVPLDPATRLAADV--GKSGTEREFRGLGCLVKITSDGIRGLYOGFSVS 181
 122 AVAQPTDVVKVRFOQ--ARAQGRYOSTVNAAYRTIAREBGRGLMKGTSPVANAALVN 180
 QY 189 AAYFGVYDTAK-----GMLPDPKXTHIVSWMIAQTVAAGVVSYPDTYRRMMQ 242
 Db 181 CAELVTVLIDALIKAMLMTDLPCHFTSAFGAGFCCTVIAS----PVDVVKIRYM--- 233
 QY 243 GRKADIMYGTVDCKRKIFRDEGKAFKGAWSNVL-R-GMGAFVLVLYDELK 298
 Db 234 --NSALQYSSAGHCALTMLQKEGPRAYKGFMPSPFLRGLGSMNVVVFVTEQLK 288

RESULT 14
 US-08-470-868A-56
 ; Sequence 56, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; * COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;
 Best Local Similarity 24.9%; Pred. No. 6e-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISTKAVAPIERVKLLQVOHASK--QIADKQYKGIIVCIVRIPEQGV 68
 Db 7 FLAGGTAACIADLTFPDLTAKVRLQIGESQGPVATVSAQYRGVMTITLMTWTEGPR 66
 QY 69 SFMRGNLANVIRYFTQALNFAKDKYKQIFLGVVDKHTQFWRYPAGNLASGAAGATSL 128
 Db 67 SLVNGLVAGLQROMSPASIRIGLYDSVKQVTPKADNSLITRILA-----GCTT 126

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Ox      243  GRGAADIMTGTAVDCEMRKIFRDEGGAKAFKAMSNVLR-GGGAFLVLYDELKVI 298
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Db      244  --NSALGQYSAGHGCHLITMLQKEGPRAYFKGMPSFRLTGSNNVVMFVYEQLRAL 298

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Search completed: December 18, 2003, 17:08:32
Job time : 23 secs

Db
191 CAELVTYDLDKDALIKANIMTDDLPGHFTSAFGAGFCTTVIAS---PVDVVKIRYM--- 243

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 41 Seconds
(without alignments)
1153.671 Million cells updates/sec

Title: US-09-185-904A-33

Perfect score: 1543
Sequence: 1 MTEQAISFANFLAGIAAA.....LRGNGAFVLVDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	AAV71033	Human adenine nucl
2	1543	100.0	298	AAV71033	Human adenine nucl
3	1543	100.0	298	AAU01200	Human adenine nucl
4	1543	100.0	298	AAU01380	Human adenine nucl
5	1543	100.0	298	AAU01427	Human adenine nucl
6	1463	94.8	298	AAU01516	Human insulin rece
7	1454	94.2	298	AAU01532	Human adenine nucl
8	1454	94.2	298	AAU01599	Human adenine nucl
9	1454	94.2	298	AAU01379	Human adenine nucl

10	1418	91.9	429	24	ABR41715
11	1412	91.5	298	19	AAW61169
12	1406	91.1	293	22	ABU53219
13	1385.5	89.8	297	21	AAV71031
14	1385.5	89.8	297	22	AAU01198
15	1385.5	89.8	297	22	AAU01378
16	1367.5	88.6	325	22	ABG15423
17	1288	83.5	263	22	ABG37056
18	1254.5	81.3	299	22	ABR66302
19	1254.5	81.3	299	22	ABR67300
20	1137.5	73.7	307	22	ABR58380
21	1119	72.5	315	22	ABU53218
22	1119	72.5	315	23	ABR21175
23	1044	67.7	228	23	ABP43205
24	981	63.6	222	23	ABP74106
25	879.5	57.0	298	22	ABG18922
26	788.5	51.1	301	23	ABP73357
27	763	49.4	484	22	ABG15422
28	763	49.4	484	22	ABG27055
29	749.5	48.6	379	24	ABR0106
30	743	48.2	379	24	ABR1267
31	742.5	48.1	346	21	AAV36577
32	742.5	48.1	346	21	AAV37261
33	742.5	48.1	346	21	AAV37264
34	742.5	48.1	346	21	AAV38460
35	742.5	48.1	363	21	AAV36576
36	742.5	48.1	363	21	AAV37260
37	742.5	48.1	363	21	AAV37263
38	742.5	48.1	363	21	AAV38459
39	742.5	48.1	381	21	AAV36575
40	742.5	48.1	381	21	AAV37259
41	742.5	48.1	381	21	AAV37262
42	742.5	48.1	381	21	AAV38465
43	742.5	48.1	992	21	AAV38462
44	742.5	48.1	1009	21	AAV38671
45	742.5	48.1	1027	21	AAV38670

ALIGNMENTS

RESULT 1	
AAV71033	
ID	AAV71033 standard; Protein: 298 AA.
AC	AAV71033;
DT	29-AUG-2000 (first entry)
XX	Human adenine nucleotide translocator ANT3.
XX	
KW	Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MP; cancer;
KW	mitochondrial permeability transition; neuroprotective; nocotropic;
KW	antiParkinsonian; cytoleptic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparasitic; cerebroprotective; therapeutic; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDP;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	
OS	Homo sapiens.
PN	W0200026370-A2.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
XX	
PR	08-SEP-1999; 99US-0393441.
XX	

PA (MITO-) MITOKOR.
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX WPI; 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46; Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Deber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX
 SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQATSPADFLAGGIAAISTKAVPIERVKLLQVQHASQIADKQYKGIIVDTIVR 60
 DB 1 MTEQATSPADFLAGGIAAISTKAVPIERVKLLQVQHASQIADKQYKGIIVDTIVR 60
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFMRYPAGNLSAG 120
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFMRYPAGNLSAG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180
 DB 121 GAAGATSLCFVYPLDPAFRTLRADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180
 QY 181 VQGIITIRAYFPGVYDTAKGMLPDPKNTHTVSMIMQVTAAGVAVSYFDPVRRMM 240
 DB 181 VQGIITIRAYFPGVYDTAKGMLPDPKNTHTVSMIMQVTAAGVAVSYFDPVRRMM 240
 QY 241 QSGRKAGDIWYTGTVDCWKRIFRDEGKAFKGMASNVLMKGMAFVLVYDELKKVI 298
 DB 241 QSGRKAGDIWYTGTVDCWKRIFRDEGKAFKGMASNVLMKGMAFVLVYDELKKVI 298

RESULT 2
 AAM39641
 ID AAM39641 standard; Protein; 298 AA.
 XX
 AC AAM39641;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 KW Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-048725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 15-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PT Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and
 the encoded polypeptides (AAM38642-AA42213) with nootropic,
 immunosuppressant and cyostatic activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 system, such as peripheral nervous injuries, peripheral neuropathy and
 localised neuropathies and central nervous system diseases, such as
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 utilisation of the activities such as: Immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQATSPADFLAGGIAAISTKAVPIERVKLLQVQHASQIADKQYKGIIVDTIVR 60
 DB 1 MTEQATSPADFLAGGIAAISTKAVPIERVKLLQVQHASQIADKQYKGIIVDTIVR 60
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFMRYPAGNLSAG 120
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFMRYPAGNLSAG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180
 DB 121 GAAGATSLCFVYPLDPAFRTLRADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180
 QY 181 VQGIITIRAYFPGVYDTAKGMLPDPKNTHTVSMIMQVTAAGVAVSYFDPVRRMM 240
 DB 181 VQGIITIRAYFPGVYDTAKGMLPDPKNTHTVSMIMQVTAAGVAVSYFDPVRRMM 240

Qy 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRMGCAFVLVYDELKKVI 298
 Db 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRMGCAFVLVYDELKKVI 298
 RESULT 3
 AAU01200
 ID AAU01200 standard; Protein; 298 AA.
 AC AAU01200;
 XX
 XX 07-SEP-2001 (first entry)
 XX
 XX Human adenine nucleotide translocator-3 (ANT-3) protein.
 DE
 XX Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX WO200132876-A2.
 PN
 XX 10-MAY-2001.
 PD
 XX 03-NOV-2000; 2000WO-US30535.
 PE
 XX 03-NOV-1999; 99US-0434354.
 PR
 XX (MITO-) MITOKOR.
 PA
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Veljcelcebi G, Davis RE;
 XX
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05903.
 XX
 PT *New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS Disclosure; Fig 2; 186pp; English.
 XX
 XX The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunction of cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTEQAISFAKDFLAGGIAAAISKTAVADIERVKLLAQVQHASKQIAADKQYKGIIVDCIVR 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MTEQAISFAKDFLAGGIAAAISKTAVADIERVKLLAQVQHASKQIAADKQYKGIIVDCIVR 60
 Qy 1 PKEGVLSFMRGNANVIRYPTQALNFAFKDKYKQIFLGVDHGTQFMWYFAGNLASG 120
 Db 61 IPKEGVLSFMRGNANVIRYPTQALNFAFKDKYKQIFLGVDHGTQFMWYFAGNLASG 120
 Qy 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFGGLDCLVKTITKSGIRGLYQGFSSVS 180
 Db 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFGGLDCLVKTITKSGIRGLYQGFSSVS 180
 Qy 181 VGGIITVRAAYFGVYDTAKGMLPDPKNTHTIVSNMIAQTVAVGVSSYPPTVRRMM 240
 Db 181 VGGIITVRAAYFGVYDTAKGMLPDPKNTHTIVSNMIAQTVAVGVSSYPPTVRRMM 240
 Qy 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRMGCAFVLVYDELKKVI 298
 Db 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRMGCAFVLVYDELKKVI 298
 RESULT 4
 AAU10380
 ID AAU10380 standard; Protein; 298 AA.
 AC AAU10380;
 XX
 XX 14-FEB-2002 (first entry)
 DT
 XX Human adenine nucleotide translocator 3 (ANT3).
 DE
 XX Human; adenine nucleotide translocator; ANT;
 KW mitochondrial matrix protein.
 KW
 XX Homo sapiens.
 OS
 XX WO200185944-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX 11-MAY-2001; 2001WO-US15416.
 PE
 XX 11-MAY-2000; 2000US-0569327.
 PR
 XX (MITO-) MITOKOR.
 PA
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 XX
 DR WPI; 2002-055598/07.
 DR N-PSDB; AAS16690.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 PS Example 3; Fig 2; 147pp; English.
 XX
 XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.

```

XX SQ Sequence 298 AA;
Query Match 100.0%; Score 1543; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAI SFADFLAGGIAAISTAVAPIERVKLLQVHASKOIADKQYKGI VDCIVR 60
DB 1 MTEBAISFADFLAGGIAAISTAVAPIERVKLLQVHASKOIADKQYKGI VDCIVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAKTRTLADVGSKGEREFRLGDCLVKTKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDPAKTRTLADVGSKGEREFRLGDCLVKTKSDGIRGLYOGFSVS 180
QY 181 VGGIIRAAVFGVYDTAKGMLPDPKXNTHIVSWMIAQTVAAGVVSYPEDTVRRMM 240
DB 181 VGGIIRAAVFGVYDTAKGMLPDPKXNTHIVSWMIAQTVAAGVVSYPEDTVRRMM 240
QY 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKAGMSVLRMGGAFFLVLYDELKQYI 298
DB 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKAGMSVLRMGGAFFLVLYDELKQYI 298

RESULT 5
ID AAM41427 standard; Protein; 323 AA.
AC AAM41427;
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 6358.
XX
XX Human; noctropic; immunosuppressant; cyostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AB, Yang Y, Zhang J,
XX Zhao QA, Zhou F, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX N-PSDB; AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -

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XX SQ Sequence 323 AA;
Query Match 100.0%; Score 1543; DB 22; Length 323;
Best Local Similarity 100.0%; Pred. No. 5,2e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAI SFADFLAGGIAAISTAVAPIERVKLLQVHASKOIADKQYKGI VDCIVR 60
DB 26 MTEQAI SFADFLAGGIAAISTAVAPIERVKLLQVHASKOIADKQYKGI VDCIVR 85
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
DB 86 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 145
QY 121 GAAGATSLCFVYPLDPAKTRTLADVGSKGEREFRLGDCLVKTKSDGIRGLYOGFSVS 180
DB 146 GAAGATSLCFVYPLDPAKTRTLADVGSKGEREFRLGDCLVKTKSDGIRGLYOGFSVS 205
QY 181 VGGIIRAAVFGVYDTAKGMLPDPKXNTHIVSWMIAQTVAAGVVSYPEDTVRRMM 240
DB 206 VGGIIRAAVFGVYDTAKGMLPDPKXNTHIVSWMIAQTVAAGVVSYPEDTVRRMM 265
QY 241 QSGRKADIMYTGTVDCWRKIFRDEGKAFKAGMSVLRMGGAFFLVLYDELKQYI 298
DB 266 QSGRKADIMYTGTVDCWRKIFRDEGKAFKAGMSVLRMGGAFFLVLYDELKQYI 323

RESULT 6
ID AAO18516 standard; Protein; 298 AA.
XX
XX AAO18516;
XX
XX 11-OCT-2002 (first entry)
XX
XX Human insulin receptor signaling modifier SEQ ID NO: 54.
XX
XX Human; insulin receptor signaling; insulin receptor signaling modifier;
XX IEM; diabetes; metabolic syndrome; antidiabetic.
XX
XX Homo sapiens.
XX
XX WO200255664-A2.
XX
XX 18-JUL-2002.
XX
XX 11-JAN-2002; 2002MO-US01048.
XX
XX 12-JAN-2001; 2001US-261226P.
XX 12-JAN-2001; 2001US-261303P.
XX 12-JAN-2001; 2001US-261304P.
XX 12-JAN-2001; 2001US-261335P.
XX 12-JAN-2001; 2001US-261336P.

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PR 12-JAN-2001; 2001US-261361P.
PR 12-JAN-2001; 2001US-261456P.
PR 12-JAN-2001; 2001US-261456P.
PR 12-JAN-2001; 2001US-261458P.
PR 12-JAN-2001; 2001US-261459P.
PR 12-JAN-2001; 2001US-261461P.
PR 12-JAN-2001; 2001US-261518P.
PR 12-JAN-2001; 2001US-261531P.
PR 12-JAN-2001; 2001US-261532P.
PR 12-JAN-2001; 2001US-261589P.
PR 12-JAN-2001; 2001US-261590P.
PR 12-JAN-2001; 2001US-261694P.
PR 12-JAN-2001; 2001US-261695P.
PR 12-JAN-2001; 2001US-261697P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Seidel-Dugan C, Ferguson KC, Kidd T,
XX
XX WPI; 2002-599664/64.
XX
XX N-PSDB; AAL46635.
XX
XX Identifying an insulin receptor signaling modulator, useful as drug
XX targets for treating diabetes or metabolic disorders, comprises
XX contacting an assay system comprising insulin receptor signaling
XX modifiers with a test agent -
XX
XX
XX Disclosure; Page 160-161; 232pp; English.
XX
XX The present invention relates to a method of identifying a candidate
XX insulin receptor (INR) signaling modulating agent, involving contacting
XX an assay system comprising an insulin receptor signaling modifier (ISM)
XX polypeptide or nucleic acid with a test agent, and detecting a test
XX agent-biased activity of the assay system. The method is useful for
XX identifying candidate INR signaling modulating agents. ISM genes may be
XX used as drug targets for treatment of disorders related to INR signaling
XX such as diabetes or metabolic syndrome. ISM nucleic acids and
XX polypeptides are useful for identifying and testing agents that modulate
XX ISM function and for other applications related to the involvement of ISM
XX in INR signaling, and for identifying subjects having a predisposition to
XX such diseases associated with INR signaling. The present sequence is an
XX ISM protein described in the exemplification of the invention.
XX
XX Sequence 298 AA:
SQ
Query Match 94.8%; Score 1463; DB 23; Length 298;
Best Local Similarity 92.9%; Pred. No. 1.8e-148;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
QY 1 MTEOATSFADKPLAGIAAATSKTAVAPIERVKLLLOVQHASKOIADKQYKGIYDCIVR 60
DB 1 MTDAAVSAKDFLAGGVAALSKTAVAPIERVKLLLOVQHASKOITADKQYKGIIDCVRR 60
QY 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
DB 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEEFEGGLDCLVYTKTSGICRGLYGGSEVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEEFEGGLDCLVYTKTSGICRGLYGGSEVS 180
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEEFEGGLDCLVYTKTSGICRGLYGGSEVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEEFEGGLDCLVYTKTSGICRGLYGGSEVS 180
QY 181 VGGIITVAAVFGVDTAKGMLPDKNTHIVVSMIAQTVAVAAGVSPYPTVARRMM 240
DB 181 VGGIITVAAVFGVDTAKGMLPDKNTHIVVSMIAQTVAVAAGVSPYPTVARRMM 240
QY 241 QSGRKGADIMYTGIVDCWRKIFRDEGGAFFKGAWSNVLRGNGAFVLYLDELK 296
DB 241 QSGRKGADIMYTGIVDCWRKIFRDEGGAFFKGAWSNVLRGNGAFVLYLDELK 296
RESULT 7
AAV71032 standard; Protein; 298 AA.

XX
AC AAY71032;
XX
DT 29-AUG-2000 (first entry)
XX
DE Human adenine nucleotide translocator ANT2.
XX
XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
XX mitochondrial permeability transition; neuroprotective; neurotropic;
XX antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
XX antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX mitochondrial encephalopathy; lactic acidosis; stroke; MTD;
XX mitochondrial diabetes and deafness; hyperproliferative disorder;
XX myoclonic epilepsy red ragged fibre syndrome.
XX
XX Homo sapiens.
XX
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1998; 98US-0185904.
XX
XX 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
XX Ghosh SS,
XX WPI; 2000-365619/31.
XX
XX N-PSDB; MAD00520.
XX
XX Recombinant construct encoding adenine nucleotide translocator
XX polypeptide, useful e.g. in screening for potential therapeutic agents
XX against mitochondrial disease -
XX
XX
XX Claim 45; Page 172-173; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
XX (ANT) proteins or ANT fusion proteins using recombinant expression
XX constructs. ANT is a nuclear encoded protein and a major component of
XX inner mitochondrial membrane. It mediates transport of adenosine
XX di/tri-phosphates across the mitochondrial inner membrane and also serves
XX as an important molecular component of the mitochondrial permeability
XX transition pore, a modulator of apoptosis. ANT is used to identify agents
XX or ligands that bind to, or interact with it. The ANT ligands are used to
XX detect or isolate ANT in a biological sample, and therapeutically for
XX regulating mitochondrial pore activity, for treating diseases associated
XX with altered mitochondrial function, including Alzheimer's, Parkinson's
XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
XX disorders, mitochondrial diabetes and deafness (MTD), and myoclonic
XX epilepsy red ragged fibre syndrome. The present sequence is an
XX adenine nucleotide translocator ANT2 from human brain.
XX
XX Sequence 298 AA;
SQ
Query Match 94.2%; Score 1454; DB 21; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MTEOATSFADKPLAGIAAATSKTAVAPIERVKLLLOVQHASKOIADKQYKGIYDCIVR 60
DB 1 MTDAAVSAKDFLAGGVAALSKTAVAPIERVKLLLOVQHASKOITADKQYKGIIDCVRR 60
QY 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
DB 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120

Db 61 IPKEQVLSPFMRGNLANVIRYPTQALNFAFKKXKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLVKTITKSDGIRGLYQGFSSVS 180
 Db 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLVKTITKSDGIRGLYQGFSSVS 180
 QY 181 VGGIITRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQTVAAGVVSYPFDVRRMM 240
 Db 181 VGGIITRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQTVAAGVVSYPFDVRRMM 240
 QY 241 QSGRKGADIMYTGTDGWRKIFDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296
 Db 241 QSGRKGADIMYTGTDGWRKIFDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296

RESULT 8
 AAU01199
 ID AAU01199 standard; Protein: 298 AA.
 AC AAU01199;
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KM Human, adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 PN WO200132876-A2.
 PD 10-MAY-2001.
 PF 03-NOV-2000; 2000WO-US30535.
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Vellicelardi G, Davis RE;
 DR WPI; 2001-2291054/30.
 DR N-PSDB; AAS05902.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC components and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 XX Sequence 298 AA;
 Query Match 94.2%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQALSFADPFLAGIAAIAISKTAVPPIERVKLLLOVHASKOIADKQYGVDCIVR 60
 Db 1 MTDALSFADPFLAGIAAIAISKTAVPPIERVKLLLOVHASKOIADKQYGVDCIVR 60
 QY 61 IPKEQVLSPFMRGNLANVIRYPTQALNFAFKKXKQIFLGVDKRTQFWRYPAGNLASG 120
 Db 61 IPKEQVLSPFMRGNLANVIRYPTQALNFAFKKXKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLVKTITKSDGIRGLYQGFSSVS 180
 Db 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLVKTITKSDGIRGLYQGFSSVS 180
 QY 181 VGGIITRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQTVAAGVVSYPFDVRRMM 240
 Db 181 VGGIITRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQTVAAGVVSYPFDVRRMM 240
 QY 241 QSGRKGADIMYTGTDGWRKIFDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296
 Db 241 QSGRKGADIMYTGTDGWRKIFDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296

RESULT 9
 AAU10379
 ID AAU10379 standard; Protein: 298 AA.
 AC AAU10379;
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 2 (ANT2).
 XX
 KM Human, adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 PN WO200185944-A2.
 PD 15-NOV-2001.
 PF 11-MAY-2001; 2001WO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 XX
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 DR WPI; 2002-055598/07.
 DR N-PSDB; AAS16689.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 PS Claim 44; Fig 2; 147pp; English.
 XX
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ADP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide.
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.
 XX
 SQ Sequence 298 AA;
 Query Match 94.2%; Score 1454; DB 23; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASQIADKQYGVDCIVR 60
 DB 1 MTDALSPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASQIADKQYGVDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQPMWRFAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQPMWRFAGNLASG 120
 QY 121 GAAGATSLCFYVPDLPARTRLAADVGSGTEREERGLDCLVKTKSGIRGLYQGSFVS 180
 DB 121 GAAGATSLCFYVPDLPARTRLAADVGSGTEREERGLDCLVKTKSGIRGLYQGSFVS 180
 QY 181 VQGIITRYAAAFYGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 240
 DB 181 VQGIITRYAAAFYGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 240
 QY 241 QSGRGADIMVTGYVDCRKRKIFRDGCGAFFFAGANSVIRMGAFVLVDELKK 296
 DB 241 QSGRGADIMVTGYVDCRKRKIFRDGCGAFFFAGANSVIRMGAFVLVDELKK 296
 DB 241 QSGRGADIMVTGYVDCRKRKIFRDGCGAFFFAGANSVIRMGAFVLVDELKK 296
 Result 10
 ABR41715
 ID ABR41715 standard; Protein; 429 AA.
 XX
 AC ABR41715;
 XX
 DT 02-JUN-2003 (first entry)
 XX
 DB Human DITHP organelle-associated protein.
 XX
 XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteomic analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;
 KW organelle-associated protein.
 KW
 XX
 OS Homo sapiens.
 XX
 XX WO200297031-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 27-MAR-2002; 2002WO-US10056.
 XX
 XX 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.
 XX
 XX (INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amesley SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;
 PI Peraletta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Uraahka ME;
 XX
 DR WPI; 2003-129518/12.
 DR N-PsDB; ACC46652.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for
 PT identifying test compound which specifically binds to a polypeptide
 PT encoded by human diagnostic and therapeutic polynucleotide, and to
 PT induce antibodies
 XX
 XX Claim 27; SEQ ID No 1250; 591pp; English.
 XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 CC to polynucleotide sequences at least 90% identical to the dithp CDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods
 CC of detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which is an organelle-
 CC associated protein.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 429 AA;
 Query Match 91.9%; Score 1418; DB 24; Length 429;
 Best Local Similarity 95.2%; Pred. No. 2e-143;
 Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;
 QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASQIADKQYGVDCIVR 60
 DB 26 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASQIADKQYGVDCIVR 85
 QY 61 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQPMWRFAGNLASG 120
 DB 86 IPKEQGVLSFWRGNLANVIRFPPTQALNFAFDKTKQIFLGVDKHTQPMWRFAGNLASG 145
 QY 121 GAAGATSLCFYVPDLPARTRLAADVGSGTEREERGLDCLVKTKSGIRGLYQGSFVS 180
 DB 146 GAAGATSLCFYVPDLPARTRLAADVGSGTEREERGLDCLVKTKSGIRGLYQGSFVS 205
 QY 181 VQGIITRYAAAFYGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 240
 DB 206 VQGIITRYAAAFYGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 265

QY 241 QSGRKGADIMYTGVDWCWRIKIFRDEGKAFKGA-W-----SNVLRNGKA 285
 Db 266 QSGRKGADIMYTGVDWCWRIKIFRDEGKAFKGSNWKQATLADALGSPSA 316

RESULT 11
 AAM61169
 ID AAM61169 standard; Protein: 298 AA.

AC AAM61169;
 XX
 DT 28-SEP-1998 (first entry)
 XX

DE Ant1 protein.

XX Ant1; Adenine nucleotide translocator; cloning; screening;
 KM DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
 KM probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 KM hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
 KM lactic acidosis; degenerative muscle disease.

XX Mus sp.

XX WO9819714-A1.

XX PD -14-MAY-1998.

XX PF 31-OCT-1997; 97WO-US19882.

XX PR 01-NOV-1996; 96US-0030017.

XX (UYEM-) UNIV EMORY.

XX Graham BC, Macgregor GR, Wallace DC;

XX WPI; 1998-286608/25.

XX N-PSDB; AAV36479.

XX Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hypertrophic
 PT cardiomyopathy in animals and to test therapeutic compositions or
 PT gene therapies

XX Disclosure; Page 39-40; 61pp; English.

XX The present sequence is the mouse Ant1 protein, the cDNA producing this

XX polypeptide is cloned by screening a mouse heart cDNA library with the

XX human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA

XX Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by

XX the Ant1 locus, a nuclear gene on chromosome 8. This protein is required

XX in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP

XX which can then be converted into ATP. An Ant1 homozygous mutant would

XX thus be defective in OXPHOS which results in disease in oxidative

XX metabolism dependent tissues. This mouse Ant1 homozygous mutant can be

XX used as a model system for fascioscapular humeral muscular dystrophy,
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of Ant1.

XX Sequence 298 AA;

Query Match 91.5%; Score 1412; DB 19; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5.4e-143;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAI SPADFLAGIAAISKTA VAPIERVKLLQVQHASKOIAADKOYKGI VDCIVR 60
 Db 1 MGQALSF LKDFLAGIAAIVSKTA VAPIERVKLLQVQHASKOISAEKQYKGI IDCIVR 60
 QY 61 IPEQGLT SWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 Db 61 IPEQGLT SWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120

QY 121 GAAGATSLCEVYPLDFARTRLAADVGSKSTEREERGLDCLVKTSDGIRGLYQGFSSVS 180
 Db 121 GAAGATSLCEVYPLDFARTRLAADVGSKSTQREFNGDGLTKTKFSKDGLKGLYQGFSSVS 180
 QY 181 VQGIITVRAAYFGVYDTAKQMLPDPKXTHIVSMMIAQVTVAVAGVSYFPDVTYRRMM 240
 Db 181 VQGIITVRAAYFGVYDTAKQMLPDPKXTHIVSMMIAQVTVAVAGVSYFPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGVDWCWRIKIFRDEGKAFKGA-SVNLRGKAFVLVYDELKKVI 298
 Db 241 QSGRKGADIMYTGVDWCWRIKIFRDEGKAFKGA-SVNLRGKAFVLVYDELKKVI 298

RESULT 12

ID ABUS3219
 XX ABUS3219 standard; Protein: 293 AA.

XX AC ABUS3219;

XX DT 14-APR-2003 (first entry)
 XX

DE Human metabolism-associated DKFzphes3_35n12 homologue #1.

XX Human; gene therapy; vaccine; disease treatment; detection.

XX Homo sapiens.

XX WO200112659-A2.

XX PD 22-FEB-2001.

XX PF 18-AUG-2000; 2000WO-IB01496.

XX PR 18-AUG-1999; 99US-0149499.

XX PR 28-SEP-1999; 99US-0156503.

XX (GERHU-) GERMAN HUMAN GENOME PROJECT.

XX Wiemann S;

XX WPI; 2001-327840/34.

XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies -

XX Example III; Page 850; 1095pp; English.

XX This invention describes novel polynucleotides and polypeptides isolated

XX from human cDNA libraries which can be used for gene therapy or in

XX vaccines. The polynucleotides of the invention and antibodies encoded by

XX them may be used in the prevention, diagnosis and treatment of diseases

XX associated with inappropriate polypeptide expression. The products of the

XX invention may also be used to identify modulators of expression and

XX activity and to down regulate expression and activity. The antibodies of

XX the invention may also be used as diagnostic agents for detecting the

XX presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.

XX Sequence 293 AA;

Query Match 91.1%; Score 1406; DB 22; Length 293;
 Best Local Similarity 90.1%; Pred. No. 2.3e-142;
 Matches 263; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

QY 5 AISPANQFLAGIAAISKTA VAPIERVKLLQVQHASKOIAADKOYKGI VDCIVR 64
 Db 1 AISPANQFLAGIAAISKTA VAPIERVKLLQVQHASKOISAEKQYKGI IDCIVR 60
 QY 65 QGTLFWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 124
 Db 61 QGTLFWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120

QY 125 ATSLCFVPLDPFARTLADVKGSGTEREPRGLGDLVKTIKSDGIRGLYQGFVSVOGI 184
 DB 121 ATSLCFVPLDPFARTLADVKGSGTEREPRGLGDLVKTIKSDGIRGLYQGFVSVOGI 180
 QY 185 IIVRAAAYGVYDTAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPPPTVRRMMQSGR 244
 DB 181 IIVRAAAYGVYDTAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPPPTVRRMMQSGR 240
 QY 245 KGADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLVLYDELKX 296
 DB 241 KGADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLVLYDELKX 292

RESULT 13
 AAY71031
 ID AAY71031 standard; Protein: 297 AA.
 AC AAY71031;
 DT 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANTL1.
 XX Human; adenine nucleotide translocator; ANTL1; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurologic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antiparietal; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS
 PN WO200026370-A2.
 PD 11-MAY-2000.
 XX 03-NOV-1999; 99WO-US25883.
 XX 03-NOV-1999; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 PA
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX WPI: 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Claim 44; Page 172; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANTL1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MTEGATSPADPFLAGGIAAIAISKTAVPIERVKLLLOVQHASKOIAADKQYKIVDCIVR 60
 DB 1 MGDHAMSFLDPLFGAAGAAVSKTAVAPIRVKLLLOVQHASKOISAEKQYKGIIDCVRR 60
 QY 1PKEQGLSPFRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDVQKHOPRPFAGNLASG 120
 DB 61 IPEQGLSPFRGNLANVIRFPPTQALNPAFKDKYKQIFLGVDVQKHOPRPFAGNLASG 120
 QY 121 GAAGATSLCFVPLDPFARTLADVKGSGTEREPRGLGDLVKTIKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVPLDPFARTLADVKGSGTEREPRGLGDLVKTIKSDGIRGLYQGFVS 179
 QY 181 VQGIIVRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPPPTVRRMM 240
 DB 180 VQGIIVRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPPPTVRRMM 239
 QY 241 QSGRKGADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLVLYDELKX 298
 DB 240 QSGRKGADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLVLYDELKX 297

RESULT 14
 AAU01198
 ID AAU01198 standard; Protein: 297 AA.
 AC AAU01198;
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS
 PN WO200132876-A2.
 PD 10-MAY-2001.
 XX 03-NOV-2000; 2000WO-US30535.
 XX 03-NOV-1999; 99US-0434354.
 XX (MITO-) MITOKOR.
 PA
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Velicelcib G, Davis RE;
 XX WPI: 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule
 XX
 PS Disclosure; Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability

CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cytochromes to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

SQ Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 22; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQATSPADFLAGIAAISTKTAVALPIERVKLLQVQASKOIADKQYKGIIDCVIR 60
 DB 1 MGDHWSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQASKOISAEKQYKGIIDCVIR 60
 QY 61 IPKEQGLTSPWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120
 DB 61 IPKEQGLTSPWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKSTGEREFGIDGLVITKTSQDGRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGKRAQREHFGIDGLVITKTSQDGRGLYQGFVS 179
 QY 181 VOGIITRYRAAFGVYDTAKGMLPDPKNTHTVSNMTAQVTAAGVSYEPDITVRRMM 240
 DB 180 VOGIITRYRAAFGVYDTAKGMLPDPKNTHTVSNMTAQVTAAGVSYEPDITVRRMM 239
 QY 241 QSGRKADIMYTGVDWCWKIFPDEGGAFFKAGMSNVLRMGAFVLVLYDEIKKYV 298
 DB 240 QSGRKADIMYTGVDWCWKIADKGAFFKAGMSNVLRMGAFVLVLYDEIKKYV 297

RESULT 15

AAU10378
 ID AAU10378 standard; Protein; 297 AA.

AC AAU10378;

DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 1 (ANT1).

KM Human; adenine nucleotide translocator; ANT;

KX mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001WO-US15416.

PR 11-MAY-2000; 2000US-0569327.

PA (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;

DR WPI; 2002-055598/07.
 DR N-PSDB; AAS16688.

PT Novel recombinant expression construct for producing adenine nucleotide

PT translocator polypeptides, comprises a regulated promoter linked to

PS Claim 44; Fig 2; 147pp; English.

CC The invention relates to a recombinant expression construct (1)

CC comprising a regulated promoter operably linked to a nucleic acid

CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT

CC proteins mediate the exchange of ATP synthesised in the mitochondrial

CC matrix for ADP in the cytosol. (1) is useful for producing recombinant

CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and

CC culturing the host cell. (1) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is

CC expressed as a fusion protein with the polypeptide of interest.

CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is

CC useful for identifying an agent that binds to an ANT polypeptide. ANT

CC ligand is useful for determining the presence of an ANT polypeptide,

CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-

CC covalently bound to a solid phase. Detectably labeled ANT ligand is also

CC useful for identifying an agent that interacts with an ANT polypeptide.

CC The present sequence represents the amino acid sequence of human ANT1.

SQ Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 23; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQATSPADFLAGIAAISTKTAVALPIERVKLLQVQASKOIADKQYKGIIDCVIR 60
 DB 1 MGDHWSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQASKOISAEKQYKGIIDCVIR 60
 QY 61 IPKEQGLTSPWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120
 DB 61 IPKEQGLTSPWRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKSTGEREFGIDGLVITKTSQDGRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGKRAQREHFGIDGLVITKTSQDGRGLYQGFVS 179
 QY 181 VOGIITRYRAAFGVYDTAKGMLPDPKNTHTVSNMTAQVTAAGVSYEPDITVRRMM 240
 DB 180 VOGIITRYRAAFGVYDTAKGMLPDPKNTHTVSNMTAQVTAAGVSYEPDITVRRMM 239
 QY 241 QSGRKADIMYTGVDWCWKIFPDEGGAFFKAGMSNVLRMGAFVLVLYDEIKKYV 298
 DB 240 QSGRKADIMYTGVDWCWKIADKGAFFKAGMSNVLRMGAFVLVLYDEIKKYV 297

Search completed: December 18, 2003, 17:10:50
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 17 Seconds
(without alignments)

824.350 Million cell updates/sec

Title: US-09-185-904A-33

Sequence: 1 MTEQALISPAKFLAGGIAA.....LRMGARVLYVDELKVTI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ,

Maximum Match 100% ,

Listing first 45 summaries

Database : Swissprot_41:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1543	100.0	298 1	ADT3_HUMAN
2	1512	98.0	298 1	ADT3_BOVIN
3	1463	94.8	298 1	ADT2_HUMAN
4	1451	94.0	298 1	ADT2_RAT
5	1445	93.6	298 1	ADT2_MOUSE
6	1424	92.3	298 1	ADT1_RAT
7	1418	91.9	298 1	ADT1_MOUSE
8	1417	91.8	297 1	ADT1_BOVIN
9	1409	91.3	298 1	ADT1_HUMAN
10	1254.5	81.3	299 1	ADT1_MOUSE
11	1204	78.0	301 1	ADT1_MOUSE
12	978	63.4	339 1	ADT1_MOUSE
13	778.5	50.5	307 1	ADT3_YEAST
14	772	50.0	308 1	ADT1_MOUSE
15	769	49.8	322 1	ADT1_MOUSE
16	768	49.8	322 1	ADT1_MOUSE
17	766	49.6	313 1	ADT1_MOUSE
18	762.5	49.4	305 1	ADT1_MOUSE
19	760.5	49.3	318 1	ADT1_MOUSE
20	750.5	48.6	385 1	ADT1_MOUSE
21	750	48.6	387 1	ADT1_MOUSE
22	748	48.5	386 1	ADT1_MOUSE
23	747	48.4	382 1	ADT1_MOUSE
24	744	48.2	387 1	ADT1_MOUSE
25	742.5	48.1	381 1	ADT1_MOUSE
26	740	48.0	331 1	ADT1_MOUSE
27	739.5	47.9	386 1	ADT1_MOUSE
28	737.5	47.8	309 1	ADT1_MOUSE
29	727	47.1	331 1	ADT1_MOUSE
30	305.5	19.8	565 1	CMC3_CAEEL
31	302	19.6	588 1	CMC3_CAEEL
32	300	19.4	330 1	GDC_BOVIN
33	299	19.4	307 1	ODC2_YEAST

34	295	19.1	678 1	CMC1_HUMAN	075746 homo sapien
35	289.5	18.6	322 1	GDC_RAT	P16261 rattus norv
36	287.5	18.6	702 1	CMC1_CAEEL	Q21153 caenorhabd
37	286	18.5	325 1	UCP5_HUMAN	095258 homo sapien
38	285	18.5	332 1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325 1	UCP5_MOUSE	Q92282 mus musculu
40	282.5	18.3	326 1	YE80_SCHPO	Q13805 echiosacch
41	280	18.1	675 1	CMC2_HUMAN	Q91800 homo sapien
42	272	17.6	315 1	MPT_HUMAN	Q91241 homo sapien
43	270	17.5	315 1	SA18_HUMAN	Q91144 homo sapien
44	265	17.2	312 1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676 1	CMC2_MOUSE	Q99x4 mus musculu

ALIGNMENTS

RESULT 1
ADT3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Mentine nucleotide translocator 3) (ANT 3).
DE SL2546 OR ANT3.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Primates; Carnivora; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";
RT J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A., Margolin J.F.;
RN Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heide F., Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L., Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bask S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W., Viallont D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E., Schnerker A., Schein J.B., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

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QY	DB	QSGKRGADIVYTGVD	CMRKIPREGGKAFPKGAMSVLV	QMGGAFLVLYDELRKYI	298
241	QSGKRGADIVYTGVD <td>CMRKIPREGGKAFPKGAMSVLV<td>QMGGAFLVLYDELRKYI<td>298</td><td></td></td></td>	CMRKIPREGGKAFPKGAMSVLV <td>QMGGAFLVLYDELRKYI<td>298</td><td></td></td>	QMGGAFLVLYDELRKYI <td>298</td> <td></td>	298	
241	QSGKRGADIVYTGVD <td>CMRKIPREGGKAFPKGAMSVLV<td>QMGGAFLVLYDELRKYI<td>298</td><td></td></td></td>	CMRKIPREGGKAFPKGAMSVLV <td>QMGGAFLVLYDELRKYI<td>298</td><td></td></td>	QMGGAFLVLYDELRKYI <td>298</td> <td></td>	298	

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